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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:06:39 ; Search time 13 Seconds  
(without alignments)  
67.365 Million cell updates/sec

Title: US-09-674-913a-1  
Perfect score: 99  
Sequence: 1 NVPGERMGRGRTSSKELA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Capext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 48531

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database :

Published.Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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3	32.3	32.3	19	10	US-09-846-258-10
4	32.3	32.3	17	10	US-09-864-761-47043
5	31.3	31.3	20	10	US-09-864-761-43265
6	31.3	31.3	20	10	US-09-876-204-3
7	31.3	31.3	23	10	US-09-955-518-14
8	29.3	29.3	9	10	US-09-845-667-22
9	29.3	29.3	10	10	US-09-867-852-95
10	29.3	29.3	17	9	US-10-056-407-23
11	29.3	29.3	19	10	US-09-847-519A-3
12	29.3	29.3	23	10	US-09-864-761-46793
13	29.3	29.3	25	10	US-09-864-761-38863
14	28.5	28.8	25	8	US-08-424-550B-242
15	28.3	28.3	14	9	US-10-056-407-26
16	28.3	28.3	21	10	US-09-775-925-3
17	27.3	27.3	8	10	US-09-845-667-35
18	27.3	27.3	11	9	US-10-108-795-26
19	27.3	27.3	11	10	US-09-845-667-1

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21	27.3	27.3	15	10	US-09-867-852-73	Sequence 73, Appl
22	27.3	27.3	16	10	US-09-987-456-13	Sequence 13, Appl
23	27.3	27.3	22	9	US-09-955-732-18	Sequence 18, Appl
24	26.3	26.3	7	10	US-09-845-667-45	Sequence 45, Appl
25	26.3	26.3	12	9	US-10-012-756-19	Sequence 19, Appl
26	26.3	26.3	17	10	US-09-864-761-40855	Sequence 40855, A
27	26.3	26.3	18	9	US-10-056-407-21	Sequence 21, Appl
28	26.3	26.3	19	10	US-09-308-150-3	Sequence 35, Appl
29	26.3	26.3	20	9	US-09-900-425A-35	Sequence 35, Appl
30	26.3	26.3	20	9	US-10-079-185-35	Sequence 35, Appl
31	26.3	26.3	20	10	US-09-876-204-4	Sequence 4, Appl1
32	26.3	26.3	20	10	US-09-876-204-5	Sequence 5, Appl1
33	26.3	26.3	20	10	US-09-884-441-400	Sequence 400, App
34	26.3	26.3	21	9	US-10-022-609-4	Sequence 4, Appl1
35	26.3	26.3	21	10	US-09-864-761-34714	Sequence 34714, A
36	26.3	26.3	21	12	US-10-079-616-20	Sequence 20, Appl
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38	26.3	26.3	25	12	US-10-066-131-29	Sequence 29, Appl
39	25.5	25.8	25	9	US-09-812-485A-34	Sequence 34, Appl
40	25.3	25.3	9	10	US-09-834-765-226	Sequence 126, App
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53	25.3	25.3	11	10	US-09-908-322-39	Sequence 39, Appl
54	25.3	25.3	11	10	US-09-839-743-23	Sequence 23, Appl
55	25.3	25.3	13	12	US-10-011-436-7	Sequence 7, Appl1
56	25.3	25.3	15	10	US-09-961-834-3	Sequence 3, Appl1
57	25.3	25.3	15	10	US-09-894-018-193	Sequence 193, App
58	25.3	25.3	15	10	US-09-894-018-193	Sequence 193, App
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69	25.3	25.3	20	10	US-09-841-132-247	Sequence 247, App
70	25.3	25.3	20	10	US-09-841-132-248	Sequence 248, App
71	25.3	25.3	22	9	US-10-125-635A-317	Sequence 317, App
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74	24.5	24.7	18	9	US-09-966-069-29	Sequence 29, Appl
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76	24.2	24.2	9	10	US-09-884-441-445	Sequence 445, App
77	24.2	24.2	10	10	US-09-779-308-561	Sequence 561, App
78	24.2	24.2	11	8	US-10-059-720-33	Sequence 501, App
79	24.2	24.2	12	9	US-08-424-550B-501	Sequence 5, Appl1
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81	24.2	24.2	13	9	US-09-966-782A-38	Sequence 38, Appl
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87	24.2	24.2	15	9	US-10-074-328-29	Sequence 29, Appl
88	24.2	24.2	15	9	US-09-940-244-24	Sequence 24, Appl
89	24.2	24.2	18	10	US-09-033-525-7	Sequence 7, Appl1
90	24.2	24.2	18	10	US-09-987-456-12	Sequence 12, Appl
91	24.2	24.2	18	10	US-10-038-612-4	Sequence 4, Appl1
92	24.2	24.2	19	9	US-10-038-612-5	Sequence 5, Appl1

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94	24	24.2	19	9	US-10-078-547-22	Sequence 22, Appl	167	22	22.2	12	10	US-09-839-743-19	Sequence 19, Appl
95	24	24.2	19	10	US-09-308-150-4	Sequence 4, Appl	168	22	22.2	12	9	US-10-045-170A-6	Sequence 6, Appl
96	24	24.2	20	9	US-09-999-745-26	Sequence 26, Appl	169	22	22.2	12	9	US-10-056-407-30	Sequence 30, Appl
97	24	24.2	20	9	US-09-554-000-10	Sequence 10, Appl	170	22	22.2	13	10	US-09-906-779-6	Sequence 6, Appl
98	24	24.2	20	10	US-09-205-658-281	Sequence 281, App	171	22	22.2	15	9	US-09-949-375A-36	Sequence 36, Appl
99	24	24.2	20	10	US-09-731-221-63	Sequence 63, Appl	172	22	22.2	15	9	US-10-211-069-9	Sequence 9, Appl
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104	24	24.2	22	10	US-09-841-132-218	Sequence 218, App	177	22	22.2	16	10	US-09-828-708-27	Sequence 27, Appl
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107	24	24.2	24	9	US-09-991-548-12	Sequence 12, Appl	180	22	22.2	17	10	US-09-839-884-15	Sequence 45, Appl
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109	24	24.2	25	10	US-09-810-310-46	Sequence 46, Appl	182	22	22.2	18	9	US-09-999-745-61	Sequence 61, Appl
110	24	24.2	25	10	US-09-864-761-46103	Sequence 46103, A	183	22	22.2	18	9	US-09-956-087-10	Sequence 10, Appl
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112	23	23.2	10	10	US-09-850-677A-6	Sequence 6, Appl	185	22	22.2	18	9	US-09-792-793A-7	Sequence 7, Appl
113	23	23.2	10	10	US-09-850-677A-6	Sequence 7, Appl	186	22	22.2	18	9	US-09-774-639-236	Sequence 236, App
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115	23	23.2	11	8	US-08-424-550B-521	Sequence 17, Appl	188	22	22.2	18	9	US-10-158-238-11	Sequence 11, Appl
116	23	23.2	12	9	US-10-171-417-4	Sequence 4, Appl	189	22	22.2	19	9	US-10-056-407-16	Sequence 16, Appl
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130	23	23.2	20	10	US-09-841-132-249	Sequence 249, App	203	22	22.2	21	9	US-09-897-778-458	Sequence 539, App
131	23	23.2	21	9	US-10-076-622-611	Sequence 611, App	204	22	22.2	21	10	US-09-864-761-42679	Sequence 42679, A
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133	23	23.2	21	10	US-09-864-761-46368	Sequence 46368, A	206	22	22.2	22	8	US-08-424-550B-558	Sequence 558, App
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135	23	23.2	22	9	US-09-852-209A-31	Sequence 31, Appl	208	22	22.2	22	12	US-10-036-869-19	Sequence 19, Appl
136	23	23.2	22	9	US-09-272-975-46	Sequence 46, Appl	209	22	22.2	23	9	US-09-747-802-21	Sequence 21, Appl
137	23	23.2	22	10	US-09-864-761-33921	Sequence 33921, A	210	22	22.2	23	12	US-10-024-935-11	Sequence 11, Appl
138	23	23.2	22	10	US-09-864-761-35816	Sequence 35816, A	211	22	22.2	24	9	US-09-983-802-524	Sequence 524, App
139	23	23.2	22	10	US-09-969-192-53	Sequence 53, Appl	212	22	22.2	24	10	US-09-864-761-33342	Sequence 33342, A
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151	22.5	22.7	22	12	US-10-095-450-36	Sequence 36, Appl	224	22	21.5	13	9	US-10-215-296-13	Sequence 13, Appl
152	22.5	22.7	5	12	US-10-036-869-17	Sequence 17, Appl	225	22	21.7	13	9	US-09-848-967-25	Sequence 25, Appl
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154	22	22.2	7	10	US-09-845-667-46	Sequence 46, Appl	227	22	21.5	24	10	US-09-864-761-36980	Sequence 36980, A
155	22	22.2	8	9	US-10-012-756-2	Sequence 2, Appl	228	22	21.2	6	10	US-09-845-667-39	Sequence 39, Appl
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157	22	22.2	8	10	US-09-904-117-4	Sequence 4, Appl	230	22	21.2	7	9	US-10-080-100-83	Sequence 83, Appl
158	22	22.2	9	9	US-10-125-635A-95	Sequence 95, Appl	231	22	21.2	7	9	US-09-185-009-132	Sequence 132, App
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243	21	21.2	9	9	US-10-143-293-8	Sequence 8, App11	316	21	21.2	20	10	US-09-308-150-16	Sequence 16, App1
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245	21	21.2	9	10	US-09-920-174-10	Sequence 10, App1	318	21	21.2	20	10	US-09-897-778-245	Sequence 245, App
246	21	21.2	9	10	US-09-778-308-389	Sequence 389, App	319	21	21.2	20	10	US-09-897-778-246	Sequence 246, App
247	21	21.2	9	10	US-09-779-308-590	Sequence 590, App	320	21	21.2	20	10	US-09-897-778-367	Sequence 367, App
248	21	21.2	9	10	US-09-779-308-672	Sequence 672, App	321	21	21.2	20	10	US-09-897-778-382	Sequence 382, App
249	21	21.2	10	10	US-09-810-310-21	Sequence 21, App1	322	21	21.2	21	9	US-09-974-879-276	Sequence 276, App
250	21	21.2	10	10	US-09-779-308-319	Sequence 319, App	323	21	21.2	21	10	US-09-864-761-33971	Sequence 33971, A
251	21	21.2	11	10	US-09-873-676-17	Sequence 17, App1	324	21	21.2	21	10	US-09-864-761-35353	Sequence 35353, A
252	21	21.2	11	10	US-09-839-743-22	Sequence 22, App1	325	21	21.2	21	10	US-09-864-761-38713	Sequence 38713, A
253	21	21.2	11	12	US-10-007-761-69	Sequence 69, App1	326	21	21.2	21	10	US-09-864-761-39245	Sequence 39245, A
254	21	21.2	11	12	US-09-981-876-257	Sequence 257, App	327	21	21.2	21	10	US-09-864-761-41061	Sequence 41061, A
255	21	21.2	12	9	US-09-962-955c-31	Sequence 31, App1	328	21	21.2	21	10	US-09-853-830-63	Sequence 41, App1
256	21	21.2	12	9	US-09-148-545-257	Sequence 257, App	329	21	21.2	21	10	US-09-853-830-85	Sequence 85, App1
257	21	21.2	12	9	US-09-903-412-118	Sequence 118, App	330	21	21.2	21	10	US-09-873-106b-22	Sequence 22, App1
258	21	21.2	12	9	US-09-791-389-172	Sequence 172, App	331	21	21.2	21	10	US-09-873-106b-22	Sequence 22, App1
259	21	21.2	12	9	US-09-791-393-172	Sequence 172, App	332	21	21.2	21	12	US-10-016-481-7	Sequence 7, App11
260	21	21.2	12	9	US-09-918-873-23	Sequence 23, App1	333	21	21.2	22	9	US-09-765-644A-33	Sequence 33, App1
261	21	21.2	12	10	US-09-096-749A-118	Sequence 118, App	334	21	21.2	22	10	US-09-765-301-33	Sequence 33, App1
262	21	21.2	13	9	US-09-291-925A-7	Sequence 7, App11	335	21	21.2	22	10	US-09-864-761-36540	Sequence 36540, A
263	21	21.2	13	9	US-09-791-389-164	Sequence 164, App	336	21	21.2	22	10	US-09-864-761-37167	Sequence 37167, A
264	21	21.2	13	9	US-09-791-393-164	Sequence 164, App	337	21	21.2	22	10	US-09-864-761-42058	Sequence 42058, A
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266	21	21.2	13	10	US-09-873-676-12	Sequence 12, App1	339	21	21.2	22	12	US-09-864-761-46463	Sequence 46463, A
267	21	21.2	13	10	US-09-791-378-252	Sequence 252, App	340	21	21.2	22	12	US-10-013-036-5	Sequence 5, App11
268	21	21.2	13	10	US-09-071-838-34	Sequence 34, App1	341	21	21.2	22	12	US-10-013-036-6	Sequence 6, App11
269	21	21.2	14	9	US-09-291-925a-5	Sequence 5, App11	342	21	21.2	22	12	US-10-013-036-8	Sequence 8, App11
270	21	21.2	14	10	US-09-935-682-44	Sequence 44, App1	343	21	21.2	22	12	US-10-013-036-9	Sequence 9, App11
271	21	21.2	15	9	US-09-927-436-8	Sequence 20, App1	344	21	21.2	23	9	US-08-809-423A-29	Sequence 29, App1
272	21	21.2	15	9	US-10-001-938-20	Sequence 31, App1	345	21	21.2	23	9	US-09-991-548-11	Sequence 11, App1
273	21	21.2	15	10	US-09-810-310-31	Sequence 29, App1	346	21	21.2	23	10	US-09-864-761-40102	Sequence 40102, A
274	21	21.2	15	10	US-09-808-037-23	Sequence 23, App1	347	21	21.2	23	10	US-09-864-761-42131	Sequence 42131, A
275	21	21.2	15	10	US-09-893-348-29	Sequence 29, App1	348	21	21.2	23	10	US-09-864-761-43526	Sequence 43526, A
276	21	21.2	15	12	US-10-041-030-16	Sequence 16, App1	349	21	21.2	24	9	US-09-788-632A-105	Sequence 105, App
277	21	21.2	16	10	US-09-842-164-7	Sequence 7, App11	350	21	21.2	24	9	US-09-974-879-457	Sequence 457, App
278	21	21.2	17	10	US-09-765-527-6	Sequence 6, App11	351	21	21.2	24	10	US-09-974-879-458	Sequence 488, App
279	21	21.2	17	10	US-09-864-761-41554	Sequence 16, App1	352	21	21.2	24	10	US-09-802-674-7	Sequence 7, App11
280	21	21.2	18	9	US-10-029-009-16	Sequence 21, App1	353	21	21.2	24	10	US-09-864-761-47573	Sequence 47573, A
281	21	21.2	18	9	US-10-117-846-21	Sequence 21, App1	354	21	21.2	25	9	US-09-875-494-4	Sequence 4, App11
282	21	21.2	18	10	US-09-864-761-35334	Sequence 35334, A	355	21	21.2	25	9	US-09-774-639-263	Sequence 263, App
283	21	21.2	18	10	US-09-864-761-43785	Sequence 43785, A	356	21	21.2	25	10	US-09-983-802-334	Sequence 334, App
284	21	21.2	19	9	US-10-001-887-110	Sequence 110, App	357	21	21.2	25	10	US-09-837-969A-54	Sequence 54, App1
285	21	21.2	19	9	US-10-029-009-28	Sequence 28, App1	358	21	21.2	25	10	US-09-837-969A-61	Sequence 61, App1
286	21	21.2	19	9	US-10-117-846-30	Sequence 30, App1	359	21	21.2	25	10	US-09-864-761-36891	Sequence 36891, A
287	21	21.2	19	9	US-10-117-846-32	Sequence 32, App1	360	21	21.2	25	10	US-09-864-761-39663	Sequence 39663, A
288	21	21.2	19	9	US-10-117-846-34	Sequence 34, App1	361	21	21.2	25	10	US-09-864-761-39667	Sequence 39667, A
289	21	21.2	19	9	US-10-018-103A-13	Sequence 13, App1	362	21	21.2	25	10	US-09-864-761-40572	Sequence 40572, A
290	21	21.2	19	10	US-09-799-875-26	Sequence 26, App1	363	21	21.2	25	10	US-09-841-321A-54	Sequence 54, App1
291	21	21.2	19	10	US-09-864-761-36523	Sequence 36523, A	364	21	21.2	25	10	US-09-841-321A-61	Sequence 61, App1
292	21	21.2	19	10	US-09-899-376-3	Sequence 3, App11	365	21	21.2	25	10	US-09-974-879-456	Sequence 456, App
293	21	21.2	19	10	US-09-308-150-1	Sequence 1, App11	366	20.5	20.7	21	10	US-09-864-761-41024	Sequence 41024, A
294	21	21.2	19	10	US-09-308-150-12	Sequence 12, App1	367	20.5	20.7	24	10	US-09-030-619-213	Sequence 213, App
295	21	21.2	19	10	US-09-308-150-13	Sequence 13, App1	368	20.5	20.7	24	10	US-09-030-619-213	Sequence 213, App
296	21	21.2	19	10	US-09-308-150-14	Sequence 14, App1	369	20.5	20.7	24	10	US-09-864-761-35141	Sequence 35141, A
297	21	21.2	20	9	US-09-954-433-1	Sequence 1, App11	370	20	20.2	6	9	US-09-917-340-2	Sequence 2, App11
298	21	21.2	20	9	US-09-984-245-305	Sequence 305, App	371	20	20.2	6	9	US-10-007-270-33	Sequence 33, App1
299	21	21.2	20	9	US-09-973-025-66	Sequence 66, App1	372	20	20.2	7	9	US-09-229-173-31	Sequence 31, App1
300	21	21.2	20	9	US-09-899-303-66	Sequence 66, App1	373	20	20.2	7	9	US-09-884-767A-112	Sequence 162, App
301	21	21.2	20	9	US-09-988-462-75	Sequence 75, App1	374	20	20.2	9	10	US-10-084-832-1	Sequence 1, App11
302	21	21.2	20	10	US-09-864-761-47004	Sequence 47004, A	375	20	20.2	9	9	US-09-767-878-14	Sequence 14, App1
303	21	21.2	20	10	US-09-864-761-48427	Sequence 48427, A	376	20	20.2	9	9	US-09-835-853-13	Sequence 15, App1
304	21	21.2	20	10	US-09-735-705-242	Sequence 242, App	377	20	20.2	9	10	US-09-835-853-15	Sequence 15, App1
305	21	21.2	20	10	US-09-735-705-245	Sequence 245, App	378	20	20.2	9	10	US-09-946-175-112	Sequence 12, App1
306	21	21.2	20	10	US-09-735-705-246	Sequence 246, App	379	20	20.2	10	9	US-09-779-308-68	Sequence 68, App
307	21	21.2	20	10	US-09-735-705-267	Sequence 367, App	380	20	20.2	10	9	US-09-955-732-16	Sequence 16, App1
308	21	21.2	20	10	US-09-735-705-367	Sequence 367, App	381	20	20.2	10	9	US-09-812-485A-40	Sequence 40, App1
309	21	21.2	20	10	US-09-918-063-51	Sequence 51, App1	382	20	20.2	10	9	US-09-899-046-219	Sequence 219, App
310	21	21.2	20	10	US-09-993-844-58	Sequence 58, App1	383	20	20.2	10	9	US-09-899-046-220	Sequence 220, App
311	21	21.2	20	10	US-09-850-716a-242	Sequence 242, App	384	20	20.2	10	9	US-09-899-046-221	Sequence 221, App
												US-09-878-281-219	Sequence 219, App

385	20	20.2	10	9	US-09-878-281-220	Sequence 220, App	458	20	20.2	18	10	US-09-864-761-42961	Sequence 42961, A
386	20	20.2	10	9	US-09-878-281-221	Sequence 221, App	459	20	20.2	18	10	US-09-864-761-42962	Sequence 42962, A
387	20	20.2	10	10	US-09-748-114-3	Sequence 3, Appl	460	20	20.2	19	9	US-10-038-612-113	Sequence 113, App
388	20	20.2	11	9	US-09-774-639-202	Sequence 202, App	461	20	20.2	19	9	US-09-812-485A-38	Sequence 38, Appl
389	20	20.2	11	10	US-09-894-018-160	Sequence 160, App	462	20	20.2	19	9	US-09-794-517-8	Sequence 8, Appl
390	20	20.2	11	10	US-09-984-056-6	Sequence 6, Appl	463	20	20.2	19	9	US-10-018-103A-10	Sequence 10, Appl
391	20	20.2	11	10	US-09-984-057-6	Sequence 6, Appl	464	20	20.2	19	10	US-09-864-761-38815	Sequence 38815, A
392	20	20.2	12	8	US-08-424-550B-429	Sequence 429, App	465	20	20.2	19	10	US-09-864-761-48146	Sequence 48146, A
393	20	20.2	12	9	US-09-981-876-266	Sequence 266, App	466	20	20.2	19	10	US-09-308-150-2	Sequence 2, Appl
394	20	20.2	12	9	US-10-094-679-7	Sequence 7, Appl	467	20	20.2	19	10	US-09-308-150-6	Sequence 6, Appl
395	20	20.2	12	9	US-09-983-802-501	Sequence 501, App	468	20	20.2	19	10	US-09-308-150-7	Sequence 7, Appl
396	20	20.2	12	9	US-09-148-545-266	Sequence 266, App	469	20	20.2	20	9	US-10-038-612-65	Sequence 65, Appl
397	20	20.2	12	10	US-09-748-114-2	Sequence 2, Appl	470	20	20.2	20	9	US-09-736-457-1835	Sequence 1835, App
398	20	20.2	12	10	US-10-057-113-18	Sequence 18, Appl	471	20	20.2	20	9	US-09-902-941-1835	Sequence 1835, App
399	20	20.2	12	12	US-10-057-113-19	Sequence 19, Appl	472	20	20.2	20	9	US-10-074-257-11	Sequence 11, Appl
400	20	20.2	12	12	US-10-057-113-20	Sequence 20, Appl	473	20	20.2	20	9	US-10-074-257-11	Sequence 11, Appl
401	20	20.2	13	9	US-09-971-980-53	Sequence 53, Appl	474	20	20.2	20	9	US-10-044-703-51	Sequence 51, Appl
402	20	20.2	13	9	US-10-015-536-19	Sequence 19, Appl	475	20	20.2	20	9	US-10-044-703-51	Sequence 51, Appl
403	20	20.2	13	9	US-10-044-703-40	Sequence 40, Appl	476	20	20.2	20	9	US-09-849-626-1835	Sequence 1835, App
404	20	20.2	13	9	US-10-215-297-14	Sequence 14, Appl	477	20	20.2	20	9	US-09-974-879-785	Sequence 285, App
405	20	20.2	13	9	US-09-362-286-13	Sequence 13, Appl	478	20	20.2	20	10	US-09-027-856-5	Sequence 5, Appl
406	20	20.2	13	9	US-09-812-485A-39	Sequence 39, Appl	479	20	20.2	20	10	US-09-731-221-64	Sequence 64, Appl
407	20	20.2	13	9	US-10-213-298-14	Sequence 14, Appl	480	20	20.2	20	10	US-09-736-076-7	Sequence 7, Appl
408	20	20.2	13	10	US-09-730-772-10	Sequence 10, Appl	481	20	20.2	20	10	US-09-735-705-243	Sequence 243, App
409	20	20.2	13	10	US-09-735-849-10	Sequence 10, Appl	482	20	20.2	20	10	US-09-735-705-377	Sequence 377, App
410	20	20.2	13	10	US-09-935-682-33	Sequence 33, Appl	483	20	20.2	20	10	US-09-841-132-262	Sequence 262, App
411	20	20.2	13	10	US-09-946-175-13	Sequence 13, Appl	484	20	20.2	20	10	US-09-308-511-14	Sequence 14, Appl
412	20	20.2	13	10	US-09-813-333-40	Sequence 40, Appl	485	20	20.2	20	10	US-09-850-716A-243	Sequence 243, App
413	20	20.2	13	10	US-09-748-114-1	Sequence 1, Appl	486	20	20.2	20	10	US-09-850-716A-377	Sequence 377, App
414	20	20.2	14	9	US-10-011-588-3	Sequence 3, Appl	487	20	20.2	20	10	US-09-813-333-51	Sequence 51, Appl
415	20	20.2	14	9	US-10-044-703-57	Sequence 57, Appl	488	20	20.2	20	10	US-09-813-333-69	Sequence 69, Appl
416	20	20.2	14	10	US-09-813-333-57	Sequence 57, Appl	489	20	20.2	20	10	US-09-897-778-243	Sequence 243, App
417	20	20.2	14	10	US-09-867-852-80	Sequence 80, Appl	490	20	20.2	20	10	US-09-897-778-377	Sequence 377, App
418	20	20.2	15	9	US-10-072-841-42	Sequence 42, Appl	491	20	20.2	21	9	US-09-974-879-410	Sequence 410, App
419	20	20.2	15	9	US-09-866-570A-29	Sequence 29, Appl	492	20	20.2	21	10	US-09-864-761-43160	Sequence 43160, A
420	20	20.2	15	9	US-10-014-485A-39	Sequence 39, Appl	493	20	20.2	21	10	US-09-864-761-43944	Sequence 43944, A
421	20	20.2	15	9	US-10-014-485A-40	Sequence 40, Appl	494	20	20.2	21	10	US-09-864-761-47384	Sequence 47384, A
422	20	20.2	15	9	US-10-153-159-40	Sequence 40, Appl	495	20	20.2	21	10	US-09-815-306-28	Sequence 28, Appl
423	20	20.2	15	9	US-09-812-485A-17	Sequence 17, Appl	496	20	20.2	21	10	US-09-835-830-66	Sequence 66, Appl
424	20	20.2	15	9	US-10-153-176-40	Sequence 40, Appl	497	20	20.2	21	9	US-09-944-849-10	Sequence 10, Appl
425	20	20.2	15	9	US-09-811-162-10	Sequence 10, Appl	498	20	20.2	22	9	US-10-038-612-115	Sequence 115, App
426	20	20.2	15	10	US-09-073-009-53	Sequence 53, Appl	499	20	20.2	22	9	US-10-038-612-115	Sequence 115, App
427	20	20.2	15	10	US-09-773-416-2	Sequence 2, Appl	500	20	20.2	22	9	US-10-038-612-115	Sequence 115, App
428	20	20.2	15	10	US-09-813-308-16	Sequence 16, Appl	501	20	20.2	22	10	US-09-815-652-41	Sequence 41, Appl
429	20	20.2	15	10	US-09-879-987-158	Sequence 158, App	502	20	20.2	22	10	US-09-864-761-37828	Sequence 37828, A
430	20	20.2	15	10	US-09-023-588-53	Sequence 53, App	503	20	20.2	22	10	US-09-864-761-37828	Sequence 37828, A
431	20	20.2	15	10	US-09-793-306-53	Sequence 53, Appl	504	20	20.2	22	12	US-10-066-751-102	Sequence 102, App
432	20	20.2	15	10	US-09-866-572A-29	Sequence 29, Appl	505	20	20.2	22	10	US-09-864-761-36147	Sequence 36147, A
433	20	20.2	15	12	US-10-139-841-39	Sequence 39, Appl	506	20	20.2	23	10	US-09-864-761-39030	Sequence 39030, A
434	20	20.2	15	12	US-10-139-841-40	Sequence 40, Appl	507	20	20.2	23	10	US-09-839-447A-111	Sequence 111, App
435	20	20.2	16	8	US-08-424-550B-196	Sequence 196, App	508	20	20.2	23	10	US-09-925-442-28	Sequence 28, Appl
436	20	20.2	17	9	US-09-972-137-2	Sequence 2, Appl	509	20	20.2	24	9	US-09-916-444A-18	Sequence 18, Appl
437	20	20.2	17	9	US-09-983-802-406	Sequence 406, App	510	20	20.2	24	9	US-09-999-774-26	Sequence 26, Appl
438	20	20.2	17	9	US-10-083-590-12	Sequence 12, Appl	511	20	20.2	24	9	US-09-788-308D-4	Sequence 4, Appl
439	20	20.2	17	9	US-09-925-287-1	Sequence 1, Appl	512	20	20.2	24	10	US-09-739-307-174	Sequence 174, App
440	20	20.2	17	9	US-10-087-345A-24	Sequence 24, Appl	513	20	20.2	24	10	US-09-864-761-33454	Sequence 33454, A
441	20	20.2	17	10	US-09-170-919-5	Sequence 5, Appl	514	20	20.2	24	10	US-09-864-761-34445	Sequence 34445, A
442	20	20.2	17	10	US-09-776-490-59	Sequence 59, Appl	515	20	20.2	24	10	US-09-864-761-34790	Sequence 34790, A
443	20	20.2	17	10	US-09-776-490-60	Sequence 60, Appl	516	20	20.2	24	10	US-09-864-761-35169	Sequence 35169, A
444	20	20.2	17	10	US-09-776-491-59	Sequence 59, Appl	517	20	20.2	24	10	US-09-864-761-39712	Sequence 39712, A
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446	20	20.2	17	10	US-09-796-138-17	Sequence 17, Appl	519	20	20.2	24	10	US-09-864-761-45210	Sequence 45210, A
447	20	20.2	17	10	US-09-864-761-44102	Sequence 44102, A	520	20	20.2	24	10	US-09-864-761-46799	Sequence 46799, A
448	20	20.2	17	10	US-09-864-761-46139	Sequence 46139, A	521	20	20.2	24	10	US-09-772-719-14	Sequence 14, Appl
449	20	20.2	17	10	US-09-880-713A-12	Sequence 12, Appl	522	20	20.2	25	9	US-09-840-377-119	Sequence 119, App
450	20	20.2	17	10	US-09-880-713A-13	Sequence 13, Appl	523	20	20.2	25	9	US-10-002-344A-265	Sequence 265, App
451	20	20.2	17	10	US-09-909-903-17	Sequence 17, Appl	524	20	20.2	25	9	US-09-896-908-8	Sequence 8, Appl
452	20	20.2	17	10	US-09-969-362-15	Sequence 15, Appl	525	20	20.2	25	10	US-09-750-726-1	Sequence 1, Appl
453	20	20.2	17	10	US-09-929-986A-1	Sequence 1, Appl	526	20	20.2	25	10	US-09-821-984-13	Sequence 13, Appl
454	20	20.2	17	10	US-09-944-849-9	Sequence 9, Appl	527	20	20.2	25	10	US-09-864-761-38859	Sequence 38859, A
455	20	20.2	17	12	US-10-066-151-103	Sequence 103, App	528	20	20.2	25	10	US-09-864-761-42618	Sequence 42618, A
456	20	20.2	18	9	US-09-983-802-497	Sequence 497, App	529	20	20.2	25	10	US-09-864-761-44918	Sequence 44918, A
457	20	20.2	18	9	US-09-882-291-36	Sequence 36, Appl	530	20	20.2	25	10	US-09-864-761-48713	Sequence 48713, A

531	20	20.2	25	10	US-09-938-315-45	Sequence 45, Appl	604	19	19.2	12	9	US-09-813-153-238	Sequence 238, App
532	20	20.2	25	12	US-10-066-151-30	Sequence 30, Appl	605	19	19.2	12	10	US-09-796-254-15	Sequence 15, Appl
533	20	20.2	25	12	US-10-035-688-2	Sequence 2, Appl	606	19	19.2	12	10	US-09-832-723-40	Sequence 40, Appl
534	19.5	19.7	21	10	US-09-861-597-12	Sequence 12, Appl	607	19	19.2	13	9	US-09-949-477-15	Sequence 15, Appl
535	19.5	19.7	14	9	US-10-072-094-109	Sequence 109, App	608	19	19.2	13	9	US-09-966-955A-33	Sequence 33, Appl
536	19.5	19.7	14	9	US-10-072-094-111	Sequence 111, App	609	19	19.2	13	10	US-09-287-849-34	Sequence 34, Appl
537	19.5	19.7	15	9	US-09-848-967-14	Sequence 14, Appl	610	19	19.2	13	10	US-09-870-725-13	Sequence 13, Appl
538	19.5	19.7	17	10	US-09-823-153-6	Sequence 6, Appl	611	19	19.2	13	10	US-09-873-637-9	Sequence 9, Appl
539	19.5	19.7	17	10	US-09-902-941-1954	Sequence 1954, Ap	612	19	19.2	13	10	US-09-873-637-9	Sequence 38, Appl
540	19.5	19.7	20	9	US-09-902-941-1955	Sequence 1955, Ap	613	19	19.2	13	10	US-09-784-887B-3	Sequence 3, Appl
541	19.5	19.7	20	9	US-09-902-941-1956	Sequence 1956, Ap	614	19	19.2	14	8	US-08-873-601-13	Sequence 13, Appl
542	19.5	19.7	22	10	US-09-995-297-43	Sequence 43, Appl	615	19	19.2	14	9	US-09-954-433-7	Sequence 7, Appl
543	19.5	19.7	22	10	US-09-995-297-44	Sequence 44, Appl	616	19	19.2	14	9	US-09-966-955A-40	Sequence 40, Appl
544	19.5	19.7	22	10	US-09-995-297-45	Sequence 45, Appl	617	19	19.2	14	9	US-09-792-630-66	Sequence 66, Appl
545	19.5	19.7	24	9	US-09-983-802-661	Sequence 661, App	618	19	19.2	14	9	US-10-080-376-66	Sequence 16, Appl
546	19.5	19.7	24	9	US-09-967-719C-11	Sequence 11, Appl	619	19	19.2	14	9	US-10-061-399-14	Sequence 14, Appl
547	19	19.2	6	9	US-09-851-026-19	Sequence 8, Appl	620	19	19.2	14	9	US-10-212-357-6	Sequence 6, Appl
548	19	19.2	7	9	US-09-811-162-8	Sequence 19, Appl	621	19	19.2	14	9	US-10-096-339-13	Sequence 13, Appl
549	19	19.2	7	9	US-09-884-429-6	Sequence 6, Appl	622	19	19.2	14	9	US-09-965-536A-46	Sequence 46, Appl
550	19	19.2	7	9	US-09-884-767A-77	Sequence 77, Appl	623	19	19.2	14	9	US-10-072-094-113	Sequence 113, App
551	19	19.2	7	9	US-09-884-767A-78	Sequence 78, Appl	624	19	19.2	14	9	US-09-791-389-161	Sequence 161, App
552	19	19.2	7	9	US-09-884-767A-135	Sequence 135, App	625	19	19.2	14	9	US-09-791-393-161	Sequence 161, App
553	19	19.2	7	10	US-09-815-330A-11	Sequence 11, Appl	626	19	19.2	14	10	US-09-157-748-20	Sequence 20, Appl
554	19	19.2	8	8	US-08-424-550B-321	Sequence 113, App	627	19	19.2	14	10	US-09-875-644-3	Sequence 8, Appl
555	19	19.2	8	8	US-10-014-485A-113	Sequence 19, Appl	628	19	19.2	14	10	US-09-873-637-8	Sequence 1, Appl
556	19	19.2	8	10	US-09-767-870-19	Sequence 128, App	629	19	19.2	14	10	US-09-916-940-17	Sequence 17, Appl
557	19	19.2	9	9	US-09-824-787B-128	Sequence 137, App	630	19	19.2	14	10	US-09-922-503-10	Sequence 10, Appl
558	19	19.2	9	9	US-09-924-400-137	Sequence 137, App	631	19	19.2	14	10	US-09-922-503-10	Sequence 15, Appl
559	19	19.2	9	9	US-09-813-718-19	Sequence 19, Appl	632	19	19.2	14	10	US-08-424-550B-326	Sequence 326, App
560	19	19.2	9	9	US-10-143-293-5	Sequence 5, Appl	633	19	19.2	15	8	US-09-826-290-149	Sequence 149, App
561	19	19.2	9	9	US-10-104-755-19	Sequence 17, Appl	634	19	19.2	15	9	US-09-826-290-149	Sequence 163, App
562	19	19.2	9	9	US-10-039-831-17	Sequence 360, App	635	19	19.2	15	9	US-09-826-290-149	Sequence 163, App
563	19	19.2	9	10	US-09-834-765-360	Sequence 457, App	636	19	19.2	15	9	US-09-175-230-1	Sequence 1, Appl
564	19	19.2	9	10	US-09-834-765-457	Sequence 457, App	637	19	19.2	15	9	US-10-010-184A-4	Sequence 4, Appl
565	19	19.2	9	10	US-09-820-936-137	Sequence 90, Appl	638	19	19.2	15	9	US-09-999-724-24	Sequence 24, Appl
566	19	19.2	9	10	US-09-820-936-137	Sequence 90, Appl	639	19	19.2	15	9	US-10-211-068-22	Sequence 22, Appl
567	19	19.2	9	10	US-09-428-755-137	Sequence 137, App	640	19	19.2	15	9	US-10-211-068-22	Sequence 23, Appl
568	19	19.2	9	10	US-09-780-668A-34	Sequence 34, Appl	641	19	19.2	15	9	US-09-791-389-293	Sequence 293, App
569	19	19.2	9	10	US-09-779-308-516	Sequence 516, App	642	19	19.2	15	9	US-09-791-393-293	Sequence 293, App
570	19	19.2	10	10	US-08-821-739A-9	Sequence 9, Appl	643	19	19.2	15	10	US-09-933-662-5	Sequence 5, Appl
571	19	19.2	10	8	US-08-854-825-41	Sequence 41, Appl	644	19	19.2	15	10	US-09-873-637A-25	Sequence 25, Appl
572	19	19.2	10	9	US-09-902-432-5	Sequence 5, Appl	645	19	19.2	15	10	US-09-326-447-15	Sequence 15, Appl
573	19	19.2	10	9	US-09-902-432-8	Sequence 8, Appl	646	19	19.2	15	10	US-09-766-779A-20	Sequence 20, Appl
574	19	19.2	10	9	US-10-012-035A-29	Sequence 29, Appl	647	19	19.2	15	10	US-09-766-779A-23	Sequence 23, Appl
575	19	19.2	10	10	US-09-834-765-504	Sequence 304, App	648	19	19.2	15	10	US-09-818-364-3	Sequence 3, Appl
576	19	19.2	10	10	US-09-845-899A-16	Sequence 16, App	649	19	19.2	15	10	US-09-791-374-441	Sequence 441, App
577	19	19.2	10	10	US-09-779-308-58	Sequence 58, App	650	19	19.2	15	12	US-10-060-714-12	Sequence 12, App
578	19	19.2	10	10	US-09-779-308-134	Sequence 134, App	651	19	19.2	16	9	US-09-731-449-53	Sequence 53, Appl
579	19	19.2	10	10	US-09-779-308-451	Sequence 451, App	652	19	19.2	16	9	US-09-922-364A-28	Sequence 28, Appl
580	19	19.2	10	10	US-09-748-114-11	Sequence 11, App	653	19	19.2	16	9	US-09-254-590-28	Sequence 28, Appl
581	19	19.2	10	12	US-10-062-257-13	Sequence 13, App	654	19	19.2	16	9	US-10-115-695-28	Sequence 28, Appl
582	19	19.2	11	8	US-08-424-550B-259	Sequence 259, App	655	19	19.2	16	9	US-09-999-724-73	Sequence 73, Appl
583	19	19.2	11	9	US-09-826-290-151	Sequence 151, App	656	19	19.2	16	9	US-10-113-794A-5	Sequence 5, Appl
584	19	19.2	11	9	US-09-826-290-299	Sequence 299, App	657	19	19.2	16	9	US-09-903-412-3	Sequence 3, Appl
585	19	19.2	11	9	US-09-851-138-109	Sequence 109, App	658	19	19.2	16	9	US-10-068-564-77	Sequence 77, Appl
586	19	19.2	11	9	US-10-012-035A-28	Sequence 28, App	659	19	19.2	16	9	US-10-116-561-28	Sequence 28, App
587	19	19.2	11	9	US-10-108-195-15	Sequence 15, App	660	19	19.2	16	9	US-10-115-671-28	Sequence 28, App
588	19	19.2	11	9	US-09-811-162-9	Sequence 9, Appl	661	19	19.2	16	10	US-09-819-308-5	Sequence 5, Appl
589	19	19.2	11	9	US-10-151-568-19	Sequence 19, Appl	662	19	19.2	16	10	US-09-096-799A-3	Sequence 3, Appl
590	19	19.2	11	10	US-09-045-620-1	Sequence 1, Appl	663	19	19.2	16	10	US-09-781-804-63	Sequence 63, Appl
591	19	19.2	11	10	US-09-826-210-4	Sequence 4, Appl	664	19	19.2	16	10	US-09-883-777-15	Sequence 15, Appl
592	19	19.2	11	10	US-09-010-714-5	Sequence 5, Appl	665	19	19.2	16	10	US-09-989-903-77	Sequence 77, Appl
593	19	19.2	11	10	US-09-734-520-69	Sequence 69, App	666	19	19.2	16	12	US-10-051-843-3	Sequence 3, Appl
594	19	19.2	11	10	US-09-791-378-434	Sequence 434, App	667	19	19.2	17	9	US-09-95A-25	Sequence 25, Appl
595	19	19.2	11	10	US-09-867-852-191	Sequence 191, App	668	19	19.2	17	10	US-09-864-761-13407	Sequence 33407, A
596	19	19.2	11	12	US-10-012-034A-69	Sequence 69, App	669	19	19.2	17	10	US-09-864-761-1654A	Sequence 36544, A
597	19	19.2	12	9	US-09-956-086-9	Sequence 9, Appl	670	19	19.2	17	10	US-09-864-761-48307	Sequence 48307, A
598	19	19.2	12	9	US-09-851-026-16	Sequence 16, Appl	671	19	19.2	17	10	US-09-326-447-17	Sequence 17, Appl
599	19	19.2	12	9	US-09-956-087-9	Sequence 9, Appl	672	19	19.2	17	10	US-09-326-447-17	Sequence 17, Appl
600	19	19.2	12	9	US-09-971-980-15	Sequence 15, Appl	673	19	19.2	18	10	US-09-805-301-92	Sequence 92, Appl
601	19	19.2	12	9	US-09-962-955C-14	Sequence 14, Appl	674	19	19.2	18	10	US-09-030-619-159	Sequence 159, App
602	19	19.2	12	9	US-09-974-879-386	Sequence 386, App	675	19	19.2	18	10	US-09-030-619-160	Sequence 160, App
603	19	19.2	12	9	US-09-325-542A-27	Sequence 27, Appl	676	19	19.2	18	10	US-09-864-761-37786	Sequence 37786, A

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679	19	19.2	18	10	US-09-734-520-7	Sequence 7, Appl1	752	19	19.2	23	10	US-09-864-761-42771	Sequence 42771, A
680	19	19.2	18	12	US-10-012-034A-7	Sequence 136, Appl1	753	19	19.2	23	10	US-09-864-761-47781	Sequence 47781, A
681	19	19.2	19	9	US-10-038-612-136	Sequence 136, App	754	19	19.2	23	10	US-09-785-632A-53	Sequence 53, Appl1
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683	19	19.2	19	10	US-09-864-761-36450	Sequence 4, Appl1	756	19	19.2	23	10	US-09-785-632A-115	Sequence 115, App
684	19	19.2	19	10	US-09-864-761-48500	Sequence 36450, A	757	19	19.2	23	10	US-09-785-632A-117	Sequence 117, App
685	19	19.2	19	10	US-09-864-761-48500	Sequence 48500, A	758	19	19.2	23	10	US-09-785-632A-147	Sequence 147, App
686	19	19.2	19	10	US-09-850-716A-388	Sequence 388, App	759	19	19.2	23	10	US-09-836-865-4	Sequence 4, Appl1
687	19	19.2	19	10	US-09-308-150-9	Sequence 308, App	760	19	19.2	23	10	US-09-918-063-36	Sequence 36, Appl1
688	19	19.2	19	10	US-09-897-778-388	Sequence 388, Appl1	761	19	19.2	23	10	US-09-928-462-27	Sequence 27, Appl1
689	19	19.2	19	10	US-09-944-849-12	Sequence 12, App	762	19	19.2	23	10	US-09-955-733-17	Sequence 17, Appl1
690	19	19.2	19	10	US-08-785-997-37	Sequence 37, Appl1	763	19	19.2	24	9	US-10-016-634A-162	Sequence 162, App
691	19	19.2	20	1	US-09-851-026-41	Sequence 41, Appl1	764	19	19.2	24	9	US-09-931-375A-79	Sequence 79, Appl1
692	19	19.2	20	9	US-09-878-603-6	Sequence 6, Appl1	765	19	19.2	24	9	US-09-974-879-385	Sequence 385, App
693	19	19.2	20	9	US-10-029-413A-27	Sequence 27, Appl1	766	19	19.2	24	9	US-09-974-879-466	Sequence 466, App
694	19	19.2	20	9	US-10-032-482-25	Sequence 25, Appl1	767	19	19.2	24	9	US-09-974-879-501	Sequence 501, App
695	19	19.2	20	9	US-10-076-622-591	Sequence 591, App	768	19	19.2	24	10	US-09-755-925-4	Sequence 5, Appl1
696	19	19.2	20	9	US-10-076-622-591	Sequence 606, App	769	19	19.2	24	10	US-09-755-925-4	Sequence 4, Appl1
697	19	19.2	20	9	US-09-387-340-37	Sequence 37, App	770	19	19.2	24	10	US-09-864-761-35428	Sequence 35428, A
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703	19	19.2	20	10	US-09-731-221-61	Sequence 62, Appl1	776	19	19.2	24	10	US-09-864-761-47741	Sequence 47741, A
704	19	19.2	20	10	US-09-864-761-36991	Sequence 36991, A	777	19	19.2	24	10	US-09-682-667-15	Sequence 15, Appl1
705	19	19.2	20	10	US-09-864-761-40262	Sequence 40262, A	778	19	19.2	24	10	US-09-847-519A-4	Sequence 4, Appl1
706	19	19.2	20	10	US-09-864-761-42503	Sequence 42503, A	779	19	19.2	24	10	US-09-964-277-17	Sequence 17, Appl1
707	19	19.2	20	10	US-09-864-761-43449	Sequence 43449, A	780	19	19.2	24	10	US-09-782-977-4	Sequence 4, Appl1
708	19	19.2	20	10	US-09-864-761-46966	Sequence 46966, A	781	19	19.2	25	9	US-09-881-572A-24	Sequence 24, Appl1
709	19	19.2	20	10	US-09-839-447A-9	Sequence 9, Appl1	782	19	19.2	25	9	US-09-991-119-1	Sequence 1, Appl1
710	19	19.2	20	10	US-09-876-221-8	Sequence 8, Appl1	783	19	19.2	25	9	US-09-798-889-169	Sequence 169, App
711	19	19.2	20	10	US-09-876-221-8	Sequence 32, Appl1	784	19	19.2	25	9	US-09-974-879-565	Sequence 565, App
712	19	19.2	20	12	US-09-757-417-32	Sequence 591, App	785	19	19.2	25	9	US-09-813-153-275	Sequence 275, App
713	19	19.2	21	9	US-09-984-245-284	Sequence 284, App	786	19	19.2	25	10	US-09-729-835-89	Sequence 89, App
714	19	19.2	21	9	US-09-965-536A-19	Sequence 19, Appl1	787	19	19.2	25	10	US-09-837-969A-22	Sequence 22, Appl1
715	19	19.2	21	9	US-09-974-879-630	Sequence 30, App	788	19	19.2	25	10	US-09-864-761-35448	Sequence 35448, A
716	19	19.2	21	9	US-09-974-879-630	Sequence 609, App	789	19	19.2	25	12	US-10-071-751-78	Sequence 78, Appl1
717	19	19.2	21	10	US-09-825-144-11	Sequence 46, Appl1	790	19	19.2	25	12	US-10-071-751-78	Sequence 78, Appl1
718	19	19.2	21	10	US-09-825-144-11	Sequence 46, Appl1	791	19	19.2	25	12	US-09-875-456A-9	Sequence 9, Appl1
719	19	19.2	21	10	US-09-864-761-36424	Sequence 36424, A	792	19	18.7	14	10	US-09-875-456A-9	Sequence 1, Appl1
720	19	19.2	21	10	US-09-864-761-41531	Sequence 41531, A	793	19	18.5	14	10	US-09-875-456A-9	Sequence 1, Appl1
721	19	19.2	21	10	US-09-864-761-48960	Sequence 48960, A	794	19	18.7	14	10	US-09-875-456A-9	Sequence 1, Appl1
722	19	19.2	21	10	US-09-864-761-48960	Sequence 48960, A	795	19	18.7	16	8	US-08-424-550B-366	Sequence 366, App
723	19	19.2	21	10	US-09-864-761-49054	Sequence 49054, A	796	19	18.7	17	9	US-10-125-470-20	Sequence 20, Appl1
724	19	19.2	21	10	US-09-853-830-42	Sequence 42, Appl1	797	19	18.5	17	9	US-10-125-470-20	Sequence 20, Appl1
725	19	19.2	21	10	US-09-853-830-90	Sequence 90, Appl1	798	19	18.5	17	9	US-09-955-504-20	Sequence 20, Appl1
726	19	19.2	21	10	US-09-853-830-105	Sequence 105, App	799	19	18.5	19	10	US-09-767-395-6	Sequence 6, Appl1
727	19	19.2	21	10	US-09-308-150-10	Sequence 10, Appl1	800	19	18.5	19	10	US-09-864-761-37377	Sequence 37377, A
728	19	19.2	21	12	US-10-036-418-1	Sequence 1, Appl1	801	19	18.5	19	10	US-09-864-761-47477	Sequence 47477, A
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731	19	19.2	22	9	US-09-924-400-132	Sequence 132, App	804	19	18.5	20	10	US-09-850-716A-410	Sequence 410, App
732	19	19.2	22	9	US-09-971-980-8	Sequence 8, Appl1	805	19	18.5	21	10	US-09-897-778-110	Sequence 110, App
733	19	19.2	22	9	US-10-001-876-131	Sequence 131, App	806	19	18.5	21	10	US-09-853-830-18	Sequence 18, App
734	19	19.2	22	9	US-10-140-372-14	Sequence 14, App	807	19	18.7	22	9	US-09-120-264-9	Sequence 9, Appl1
735	19	19.2	22	9	US-09-974-879-602	Sequence 602, App	808	19	18.5	22	9	US-09-861-668-22	Sequence 22, Appl1
736	19	19.2	22	9	US-10-024-450-7	Sequence 7, Appl1	809	19	18.5	22	10	US-09-995-297-46	Sequence 46, App
737	19	19.2	22	9	US-10-092-750-47	Sequence 47, Appl1	810	19	18.7	22	10	US-09-995-297-46	Sequence 46, App
738	19	19.2	22	10	US-09-780-070-34	Sequence 34, Appl1	811	19	18.5	24	9	US-10-207-951-19	Sequence 19, Appl1
739	19	19.2	22	10	US-09-799-875-31	Sequence 31, Appl1	812	19	18.7	24	9	US-09-185-908-37	Sequence 37, Appl1
740	19	19.2	22	10	US-09-864-761-33352	Sequence 33352, A	813	19	18.2	5	9	US-09-185-908-158	Sequence 158, App
741	19	19.2	22	10	US-09-864-761-33128	Sequence 33128, A	814	19	18.2	5	12	US-10-029-756-25	Sequence 25, Appl1
742	19	19.2	22	10	US-09-864-761-39519	Sequence 39519, A	815	19	18.2	6	9	US-09-486-734A-24	Sequence 24, Appl1
743	19	19.2	22	10	US-09-864-761-39519	Sequence 39519, A	816	19	18.2	6	9	US-09-185-908-36	Sequence 36, Appl1
744	19	19.2	22	10	US-09-864-761-42066	Sequence 42066, A	817	19	18.2	6	9	US-09-185-908-40	Sequence 40, App
745	19	19.2	22	10	US-09-810-936-132	Sequence 132, App	818	19	18.2	6	9	US-09-185-908-129	Sequence 129, App
746	19	19.2	22	10	US-09-429-755-132	Sequence 132, App	819	19	18.2	6	9	US-09-185-908-159	Sequence 159, App
747	19	19.2	22	10	US-09-747-029A-22	Sequence 12, App	820	19	18.2	6	9	US-09-185-908-161	Sequence 161, App
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824	18	18.2	6	10	US-09-364-597A-23	Sequence 23, Appl	897	18	18.2	9	10	US-09-780-053-563	Sequence 563, App
825	18	18.2	6	10	US-09-922-261-443	Sequence 443, App	898	18	18.2	9	10	US-09-780-053-652	Sequence 652, App
826	18	18.2	6	10	US-09-177-843-2	Sequence 2, Appl1	899	18	18.2	9	10	US-09-753-831-18	Sequence 18, Appl
827	18	18.2	7	8	US-08-987-756-3	Sequence 3, Appl1	900	18	18.2	9	10	US-09-753-831-19	Sequence 19, Appl
828	18	18.2	7	9	US-10-014-485A-133	Sequence 133, App	901	18	18.2	9	10	US-09-746-945-6	Sequence 6, Appl1
829	18	18.2	7	9	US-09-185-908-39	Sequence 39, Appl	902	18	18.2	9	12	US-10-062-257-12	Sequence 12, Appl
830	18	18.2	7	9	US-09-185-908-114	Sequence 114, Appl	903	18	18.2	9	12	US-10-042-202-12	Sequence 12, Appl
831	18	18.2	7	9	US-09-185-908-114	Sequence 114, App	904	18	18.2	10	9	US-10-040-572-5	Sequence 7, Appl1
832	18	18.2	7	9	US-09-185-908-123	Sequence 123, App	905	18	18.2	10	9	US-09-902-432-73	Sequence 23, Appl
833	18	18.2	7	9	US-09-185-908-141	Sequence 141, App	906	18	18.2	10	9	US-10-000-273-8	Sequence 8, Appl1
834	18	18.2	7	9	US-09-185-908-150	Sequence 150, App	907	18	18.2	10	9	US-10-007-270-36	Sequence 36, Appl
835	18	18.2	7	9	US-09-185-908-160	Sequence 160, App	908	18	18.2	10	9	US-10-007-270-37	Sequence 37, Appl
836	18	18.2	7	9	US-09-185-908-162	Sequence 162, App	909	18	18.2	10	9	US-09-981-876-226	Sequence 226, App
837	18	18.2	7	9	US-09-884-767A-29	Sequence 29, Appl	910	18	18.2	10	9	US-09-185-908-119	Sequence 119, App
838	18	18.2	7	9	US-09-884-767A-68	Sequence 68, Appl	911	18	18.2	10	9	US-09-185-908-128	Sequence 128, App
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840	18	18.2	7	10	US-09-732-411-3	Sequence 3, Appl1	913	18	18.2	10	9	US-09-185-908-146	Sequence 146, App
841	18	18.2	7	10	US-09-845-667-36	Sequence 36, Appl	914	18	18.2	10	9	US-09-185-908-155	Sequence 155, App
842	18	18.2	7	10	US-09-845-667-37	Sequence 37, Appl	915	18	18.2	10	9	US-09-860-395-5	Sequence 5, Appl1
843	18	18.2	7	10	US-09-845-667-40	Sequence 40, Appl	916	18	18.2	10	9	US-09-860-395-5	Sequence 5, App
844	18	18.2	7	10	US-09-845-667-41	Sequence 41, Appl	917	18	18.2	10	9	US-09-148-545-226	Sequence 226, App
845	18	18.2	7	10	US-09-845-667-52	Sequence 52, Appl	918	18	18.2	10	9	US-09-799-250-275	Sequence 275, App
846	18	18.2	7	10	US-09-845-667-55	Sequence 55, Appl	919	18	18.2	10	9	US-09-799-250-372	Sequence 372, App
847	18	18.2	8	1	US-08-779-457-39	Sequence 39, Appl	920	18	18.2	10	9	US-09-894-912A-21	Sequence 21, Appl
848	18	18.2	8	1	US-10-014-485A-49	Sequence 49, Appl	921	18	18.2	10	9	US-09-977-797A-110	Sequence 130, App
849	18	18.2	8	9	US-10-014-485A-50	Sequence 50, Appl	922	18	18.2	10	9	US-09-040-518-22	Sequence 22, Appl
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851	18	18.2	8	9	US-09-185-908-42	Sequence 42, Appl	924	18	18.2	10	10	US-09-731-221-6	Sequence 6, Appl1
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858	18	18.2	8	9	US-09-185-908-144	Sequence 144, App	931	18	18.2	10	10	US-09-732-411-11	Sequence 11, Appl
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860	18	18.2	8	9	US-09-185-908-153	Sequence 153, App	933	18	18.2	10	10	US-09-780-053-74	Sequence 74, Appl
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862	18	18.2	8	9	US-10-214-802-39	Sequence 39, Appl	935	18	18.2	10	10	US-09-780-053-194	Sequence 194, App
863	18	18.2	8	9	US-09-759-130B-434	Sequence 434, App	936	18	18.2	10	10	US-09-780-053-503	Sequence 403, App
864	18	18.2	8	9	US-10-033-350-3	Sequence 3, Appl1	937	18	18.2	10	10	US-09-780-053-502	Sequence 502, App
865	18	18.2	8	10	US-09-056-160B-19	Sequence 19, Appl	938	18	18.2	10	10	US-09-780-053-582	Sequence 582, App
866	18	18.2	8	10	US-09-767-870-16	Sequence 16, Appl	939	18	18.2	10	10	US-09-780-053-614	Sequence 614, App
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875	18	18.2	9	9	US-09-185-908-137	Sequence 127, App	948	18	18.2	11	10	US-09-823-649A-11	Sequence 11, Appl
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878	18	18.2	9	9	US-09-185-908-143	Sequence 143, App	951	18	18.2	11	10	US-09-777-710A-6	Sequence 6, Appl1
879	18	18.2	9	9	US-09-185-908-145	Sequence 145, App	952	18	18.2	11	10	US-09-823-829-36	Sequence 36, Appl
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881	18	18.2	9	9	US-09-185-908-154	Sequence 154, App	954	18	18.2	11	10	US-09-867-852-110	Sequence 110, App
882	18	18.2	9	9	US-09-010-552-8	Sequence 8, Appl1	955	18	18.2	11	10	US-09-867-852-113	Sequence 113, App
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884	18	18.2	9	10	US-09-765-086-191	Sequence 191, App	957	18	18.2	11	10	US-09-867-852-200	Sequence 200, App
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887	18	18.2	9	10	US-09-834-765-29	Sequence 29, Appl	960	18	18.2	11	12	US-08-927-939-75	Sequence 75, Appl
888	18	18.2	9	10	US-09-780-053-37	Sequence 37, Appl	961	18	18.2	12	8	US-09-812-485A-19	Sequence 19, Appl
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894	18	18.2	9	10	US-09-780-053-420	Sequence 420, App	967	18	18.2	12	10	US-09-742-375-4	Sequence 4, Appl1
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975 18 18.2 12 10 US-09-922-261-439 Sequence 25, Appl1  
976 18 18.2 12 10 US-09-902-741-10 Sequence 10, Appl1  
977 18 18.2 13 9 US-10-216-408-25 Sequence 67, Appl1  
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979 18 18.2 13 9 US-10-067-790-58 Sequence 58, Appl1  
980 18 18.2 13 9 US-09-839-383-58 Sequence 58, Appl1  
981 18 18.2 13 9 US-09-966-422B-37 Sequence 37, Appl1  
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984 18 18.2 13 9 US-10-018-103A-1 Sequence 1, Appl1  
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987 18 18.2 13 10 US-09-761-636A-16 Sequence 16, Appl1  
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989 18 18.2 13 10 US-09-873-676-26 Sequence 26, Appl1  
990 18 18.2 13 10 US-09-865-018-27 Sequence 26, Appl1  
991 18 18.2 13 10 US-09-865-018-27 Sequence 27, Appl1  
992 18 18.2 13 10 US-09-981-194-11 Sequence 11, Appl1  
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994 18 18.2 13 10 US-09-981-194-26 Sequence 29, Appl1  
995 18 18.2 13 12 US-10-001-843-152 Sequence 152, Appl1  
996 18 18.2 14 9 US-09-956-086-7 Sequence 7, Appl1  
997 18 18.2 14 9 US-09-966-955A-42 Sequence 42, Appl1  
998 18 18.2 14 9 US-09-999-745-58 Sequence 58, Appl1  
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## ALIGNMENTS

RESULT 1  
US-09-808-972-11  
Sequence 11, Application US/09808972  
Patent No. US20020064832A1  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.  
APPLICANT: Topouzis, Stavros G.  
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE  
FILE REFERENCE: 00-79  
CURRENT APPLICATION NUMBER: US/09/808,972  
CURRENT FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: US 60/235,295  
PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/564,595  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: US 60/180,169  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/164,463  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: US 60/132,250  
PRIOR FILING DATE: 1999-05-03  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 11  
LENGTH: 24  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: peptide  
US-09-808-972-11  
Query Match 33.8%; Score 33.5; DB 10; Length 24;  
Best local Similarity 58.3%; Pred. No. 45;  
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

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Db 4 PGHKRGRKAKT 15

RESULT 2  
US-09-864-761-42868  
Sequence 42868, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm1ca-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
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PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 42868  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
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OTHER INFORMATION: MAP TO AL121654.1  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.98  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.91  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.87  
US-09-864-761-42868



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Best Local Similarity 58.3%; Pred. No. 44;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 5 VGRHRCCKTA 16

## RESULT 3

US-09-846-258-10  
; Sequence 10, Application US/09846258  
; Patent No. US20020006640A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: Uteroglobulin-Like Polynucleotides, Polypeptides, and Antibodies  
; FILE REFERENCE: PM023p1  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: PCT/US00/30326  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: 60/163,395  
; PRIOR FILING DATE: 1999-11-04  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-846-258-10

Query Match 32.3%; Score 32; DB 10; Length 17;  
Best Local Similarity 55.6%; Pred. No. 53;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db 9 PNHENIGPG 17

## RESULT 4

US-09-864-761-47043  
; Sequence 47043, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David K.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
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; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30  
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; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 47043  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens

FEATURE:  
; OTHER INFORMATION: MAP TO AC005868.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.53  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.59  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.63

US-09-864-761-47043

Query Match 32.3%; Score 32; DB 10; Length 19;  
Best Local Similarity 46.2%; Pred. No. 60;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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Db 3 POHRHLEGDS 15

## RESULT 5

US-09-864-761-43265  
; Sequence 43265, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David K.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665

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? PRIOR APPLICATION NUMBER: PCT/US01/00668
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00663
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00662
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00661
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 09/608,408
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: US 09/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 43265
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
? OTHER INFORMATION: MAP TO AL023513.1
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
? OTHER INFORMATION: EST_HUMAN HIT: F05756.1, EVALU05.00e-06
US-09-864-761-43265

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INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-845-667-22

Query Match 29.3%; Score 29; DB 10; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.8e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 GGRGRTSS 15  
111111  
DB 1 GRARTSS 7

## RESULT 9

US-09-867-852-95  
Sequence 95, Application US/09867852  
Patent No. US20020147324A1  
GENERAL INFORMATION:  
APPLICANT: Ausubel, Frederick M.  
APPLICANT: Staskawicz, Brian J.  
APPLICANT: Brent, Andrew F.  
APPLICANT: Dahlbeck, Douglas  
APPLICANT: Katagiri, Fumitaki  
APPLICANT: Kunkel, Barbara N.  
APPLICANT: Mindrinos, Michael N.  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND  
TITLE OF INVENTION: DETECTION METHODS  
FILE REFERENCE: 00786/254002  
CURRENT FILING DATE: 2001-05-29  
CURRENT APPLICATION NUMBER: US/09/867,852  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: 08/310,912  
PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 95  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-09-867-852-95

Query Match 29.3%; Score 29; DB 10; Length 10;  
Best Local Similarity 83.3%; Pred. No. 89;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 VPGHER 7  
111111  
DB 3 VPGHTR 8

RESULT 10  
US-10-056-407-23  
Sequence 23, Application US/10056407  
Patent No. US20020165355A1  
GENERAL INFORMATION:  
APPLICANT: MEHENS, LYDIE  
APPLICANT: LUHRMANN, REINHARD GEORGE  
APPLICANT: UNION, ANN  
APPLICANT: RAYACKERS, JOSEPH  
TITLE OF INVENTION: METHYLATED, SMD HOMOLOGOUS PEPTIDES, REACTIVE WITH THE ANTIBODIES  
TITLE OF INVENTION: SERA OF LYING BEINGS AFFECTED WITH SYSTEMIC LUPUS ERYTHEMATOSUS  
FILE REFERENCE: INNS-011-1  
CURRENT APPLICATION NUMBER: US/10/056,407

CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: US 09/297,981  
PRIOR FILING DATE: 1999-05-10  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 23  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-10-056-407-23

Query Match 29.3%; Score 29; DB 9; Length 17;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 GHERMGGR 12  
111111  
DB 7 GNGRGGR 15

## RESULT 11

US-09-847-519A-3  
Sequence 3, Application US/09847519A  
Patent No. US20020102693A1  
GENERAL INFORMATION:  
APPLICANT: Luche, Ralf M.  
APPLICANT: Wei, Bo  
TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE  
FILE REFERENCE: 200125,422  
CURRENT APPLICATION NUMBER: US/09/847,519A  
CURRENT FILING DATE: 2001-05-01  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: DSP-14 active site  
US-09-847-519A-3

Query Match 29.3%; Score 29; DB 10; Length 19;  
Best Local Similarity 46.7%; Pred. No. 1.8e+02;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 5 HERMGRTSSKELA 19  
111111  
DB 2 HCVMGRSRATLVLA 16

RESULT 12  
US-09-864-761-46793  
Sequence 46793, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 46793  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AP000177.1  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76  
US-09-664-761-46793

Query Match  
Best Local Similarity 29.3%; Score 29; DB 10; Length 23;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VPGHRMG 9  
Db 13 IPAHYRLG 20

RESULT 13  
US-09-864-761-38863  
Sequence 38863, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: A601000000-1  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 38863  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL035681.13  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 3.3  
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.3  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7  
OTHER INFORMATION: EST\_HUMAN HIT: BF346206.1, EVALUE 5.00e-06  
US-09-864-761-38863

Query Match  
Best Local Similarity 29.3%; Score 29; DB 10; Length 25;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MGRGRTS 14  
Db 17 LGGGRTS 23

RESULT 14  
US-08-424-550B-242  
Sequence 242, Application US/08424550B  
Patent No. US20020119447A1  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAMSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHROFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAMMAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
 STREET: 100 ABBOTT PARK ROAD  
 CITY: ABBOTT PARK  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,550B  
 FILING DATE:  
 CLASSIFICATION: 435435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: POREMSKI, PRISCILLA E.  
 REGISTRATION NUMBER: 33,207  
 REFERENCE/DOCKET NUMBER: 5527.PC.01  
 TELEPHONE: 708-937-6365  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: 708-938-2623  
 INFORMATION FOR SEQ ID NO: 242:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-424-550B-242

Query Match 28.8%; Score 28.5; DB 8; Length 25;  
 Best Local Similarity 47.1%; Pred. No. 2.8e+02;  
 Matches 8; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 3 PGERMGRRTSSKELA 19  
 |||:|:|:|  
 Db 4 PGRRLTG-GLSESDRLA 19

RESULT 15  
 US-10-056-407-26  
 ; Sequence 26, Application US/10056407  
 ; Patent No. US2002016355A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MEHENS, LYDIE  
 ; APPLICANT: LUHMANN, REINHARD GEORGE  
 ; APPLICANT: UNION, ANN  
 ; APPLICANT: RAYMAKERS, JOSEPH  
 ; TITLE OF INVENTION: SERA OF LIVING BEINGS AFFECTED WITH SYSTEMIC LUPUS ERYTHEMATOSUS  
 ; FILE REFERENCE: INNS:011-1  
 ; CURRENT APPLICATION NUMBER: US/10/056,407  
 ; PRIOR FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: US 09/297,981  
 ; FILING DATE: 1999-05-10  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 26  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Peptide  
 ; US-10-056-407-26

Query Match 28.3%; Score 28; DB 9; Length 14;  
 Best Local Similarity 62.5%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 GHERMGRG 11  
 |:|:|  
 Db 1 GDDRGRG 8

RESULT 16  
 US-09-775-925-3  
 ; Sequence 3, Application US/09775925  
 ; Patent No. US20010049358A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lucche, Ralf M.  
 ; APPLICANT: Wei, Bo  
 ; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY  
 ; FILE REFERENCE: 200125.420  
 ; CURRENT APPLICATION NUMBER: US/09/775,925  
 ; FILING DATE: 2001-02-01  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 21  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-09-775-925-3

Query Match 28.3%; Score 28; DB 10; Length 21;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+02;  
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 5 HERMGRRTSSKELA 19  
 |:|:|:|:|  
 Db 4 HCMGVSRASSTVIA 18

RESULT 17  
 US-09-845-667-35  
 ; Sequence 35, Application US/09845667  
 ; Patent No. US2002006522A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cohen, Philip  
 ; APPLICANT: Alessi, Dario  
 ; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD  
 ; FOR AGENTS  
 ; NUMBER OF SEQUENCES: 58  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Braman & Rogalskyj, LLP  
 ; STREET: P.O. Box 352  
 ; CITY: Canandaigua  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 14424-0352  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION NUMBER: US/09/845,667  
 ; FILING DATE: 30-Apr-2001  
 ; CLASSIFICATION: <unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 09/091,763  
 ; FILING DATE: 19-JUN-1998  
 ; APPLICATION NUMBER: PCT/GB96/03186  
 ; FILING DATE: 20-DEC-1996  
 ; APPLICATION NUMBER: GB 9526083.2  
 ; FILING DATE: 20-DEC-1995  
 ; APPLICATION NUMBER: GB 9610272.8  
 ; FILING DATE: 16-MAY-1996  
 ; APPLICATION NUMBER: GB 9615066.9  
 ; FILING DATE: 18-JUL-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Braman, Susan J  
 ; REGISTRATION NUMBER: 34,103  
 ; REFERENCE/DOCKET NUMBER: 002.00041  
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 716-393-3002  
TELEFAX: 716-393-3001  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-845-667-35

Query Match 27.3%; Score 27; DB 10; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.8e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 GGRPTSS 15  
DB 1 GGRPTSS 7

RESULT 18  
US-10-108-795-26  
Sequence 26, Application US/10108795  
Publication No. US2003003633A1  
GENERAL INFORMATION:  
APPLICANT: Hemmings, Brian A  
TITLE OF INVENTION: Calcium Regulated Kinase  
FILE REFERENCE: 30110  
CURRENT APPLICATION NUMBER: US/10/108,795  
PRIOR FILING DATE: 2002-03-28  
PRIOR APPLICATION NUMBER: 09/133,062  
PRIOR FILING DATE: 1998-08-12  
PRIOR APPLICATION NUMBER: GB 9717089.8  
PRIOR FILING DATE: 1997-08-12  
PRIOR APPLICATION NUMBER: GB 9717499.9  
PRIOR FILING DATE: 1998-08-19  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 26  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide  
-10-108-795-26

Query Match 27.3%; Score 27; DB 9; Length 11;  
Best Local Similarity 85.7%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 GGRPTSS 15  
DB 1 GGRPTSS 7

RESULT 19  
US-09-845-667-1  
Sequence 1, Application US/09845667  
Patent No. US20020065221A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Phillip  
Alesci, Dario  
Cross, Datten  
TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD  
FOR AGENTS  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Braham & Rogalsky, LLP  
STREET: P. O. Box 352  
CITY: Canandaigua

STATE: New York  
COUNTRY: USA  
ZIP: 14424-0352  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/845,667  
FILING DATE: 30-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/091,763  
FILING DATE: 19-JUN-1998  
APPLICATION NUMBER: PCT/GB96/03186  
FILING DATE: 20-DEC-1996  
APPLICATION NUMBER: GB 9526083.2  
FILING DATE: 20-DEC-1995  
APPLICATION NUMBER: GB 9610272.8  
FILING DATE: 16-MAY-1996  
APPLICATION NUMBER: GB 9615066.9  
FILING DATE: 18-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Braham, Susan J  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 002,00041  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-393-3001  
TELEFAX: 716-393-3002  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-845-667-1

Query Match 27.3%; Score 27; DB 10; Length 11;  
Best Local Similarity 85.7%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 GGRPTSS 15  
DB 1 GGRPTSS 7

RESULT 20  
US-09-966-782A-39  
Sequence 39, Application US/09966782A  
Publication No. US20030022183A1  
GENERAL INFORMATION:  
APPLICANT: Battaglini, P.  
Feder, J. N.  
APPLICANT: Mintier, G.  
APPLICANT: Ramanathan, C. S.  
APPLICANT: Westphal, R.  
APPLICANT: Hawken, D. R.  
APPLICANT: Cacace, A.  
APPLICANT: Barber, L.  
APPLICANT: Kornacker, M. G.  
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY7,  
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY7,  
FILE REFERENCE: D0044NP  
CURRENT APPLICATION NUMBER: US/09/966,782A  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/235,731  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/268,580  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: 60/315,423

;; PRIOR FILING DATE: 2001-08-28  
;; NUMBER OF SEQ ID NOS: 64  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 39  
;; LENGTH: 13  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-966-782A-39

Query Match 27.3%; Score 27; DB 9; Length 13;  
Best Local Similarity 40.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 GGRGRTSSKEL 18  
DB 2 GKGRTERKAEI 11

RESULT 21

US-09-867-852-73  
;; Sequence 73, Application US/09867852  
;; Patent No. US2002014732A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ausubel, Frederick M.  
;; APPLICANT: Staskawicz, Brian J.  
;; APPLICANT: Brent, Andrew F.  
;; APPLICANT: Dahlbeck, Douglas  
;; APPLICANT: Katagiri, Fumiaki  
;; APPLICANT: Kunkel, Barbara N.  
;; APPLICANT: Mandinos, Michael N.  
;; APPLICANT: Yu, Guo-Liang  
;; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND  
;; FILE REFERENCE: 00786/254002  
;; CURRENT APPLICATION NUMBER: US/09/867,852  
;; CURRENT FILING DATE: 2001-05-29  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13  
;; NUMBER OF SEQ ID NOS: 208  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 73  
;; LENGTH: 15  
;; TYPE: PRT  
;; ORGANISM: Arabidopsis thaliana  
US-09-867-852-73

Query Match 27.3%; Score 27; DB 10; Length 15;  
Best Local Similarity 41.7%; Pred. No. 2.8e+02;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GHERMGRTSS 15  
DB 3 GHRUGENWSSS 14

RESULT 22  
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;; Sequence 13, Application US/09987456  
;; Patent No. US20020123057A1  
;; GENERAL INFORMATION:  
;; APPLICANT: University of Rochester  
;; APPLICANT: Zauderer, Maurice  
;; APPLICANT: Ernest S. Smith  
;; TITLE OF INVENTION: In Vitro Methods of Producing And Selecting  
;; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells  
;; FILE REFERENCE: 1821.0070004

;; CURRENT APPLICATION NUMBER: US/09/987,456  
;; CURRENT FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/271,424  
;; PRIOR FILING DATE: 2001-02-27  
;; PRIOR APPLICATION NUMBER: 60/262,067  
;; PRIOR FILING DATE: 2001-01-18  
;; PRIOR APPLICATION NUMBER: 60/298,087  
;; PRIOR FILING DATE: 2001-06-15  
;; PRIOR APPLICATION NUMBER: 60/249,268  
;; PRIOR FILING DATE: 2000-11-17  
;; NUMBER OF SEQ ID NOS: 147  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 13  
;; LENGTH: 16  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: linker peptide  
US-09-987-456-13

Query Match 27.3%; Score 27; DB 10; Length 16;  
Best Local Similarity 66.7%; Pred. No. 3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GRTSSKELA 19  
DB 3 GSVSSEELA 11

RESULT 23  
US-09-955-732-18  
;; Sequence 18, Application US/09955732  
;; Publication No. US20020182203A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Luche, Ralf M.  
;; APPLICANT: Wei, Bo  
;; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE  
;; FILE REFERENCE: 200125.433  
;; CURRENT APPLICATION NUMBER: US/09/955,732  
;; CURRENT FILING DATE: 2001-09-18  
;; NUMBER OF SEQ ID NOS: 27  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 18  
;; LENGTH: 22  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-955-732-18

Query Match 27.3%; Score 27; DB 9; Length 22;  
Best Local Similarity 40.0%; Pred. No. 4.2e+02;  
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 5 HERMGRTSSKELA 19  
DB 4 HCKMGVRSATATVLA 18

RESULT 24  
US-09-845-667-45  
;; Sequence 45, Application US/09845667  
;; Patent No. US20020065221A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Cohen, Phillip  
;; APPLICANT: Alessi, Dario  
;; APPLICANT: Cross, Darren  
;; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD  
;; FOR AGENTS  
;; NUMBER OF SEQUENCES: 58  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Braman & Rogalskyj, LLP  
;; STREET: P.O. Box 352  
;; CITY: Canandaigua  
;; STATE: New York

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? COUNTRY: USA
? ZIP: 14424-0352
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/845,667
? FILING DATE: 30-Apr-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 09/091,763
? FILING DATE: 19-JUN-1998
? APPLICATION NUMBER: PCT/GB96/03186
? FILING DATE: 20-DEC-1996
? APPLICATION NUMBER: GB 9526083.2
? FILING DATE: 20-DEC-1995
? APPLICATION NUMBER: GB 9610272.8
? FILING DATE: 16-MAY-1996
? APPLICATION NUMBER: GB 9615066.9
? FILING DATE: 18-JUL-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Braham, Susan J
? REGISTRATION NUMBER: 34,103
? REFERENCE/DOCKET NUMBER: 002,00041
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 716-393-3002
? TELEFAX: 716-393-3001
? INFORMATION FOR SEQ ID NO: 45:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-845-667-45

Query Match      26.3%; Score 26; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 RGRSSK 16
DB 1 RPRSSK 7

ULF 25
us-10-012-756-19
? Sequence 19, Application US/10012756
? Patent No. US20020164355A1
? GENERAL INFORMATION:
? APPLICANT: John B. Harley and Judith A. James
? TITLE OF INVENTION: Diagnostics And Therapy Of Epstein-Barr
? Virus In Autoimmune Disorders
? NUMBER OF SEQUENCES: 38
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Patrea L. Pabst
? STREET: 2800 One Atlantic Center
? CITY: Atlanta
? STATE: Georgia
? COUNTRY: USA
? ZIP: 30306-3450
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/012,756
? FILING DATE: 24-Oct-2001

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? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/781,296
? FILING DATE: 13-JAN-1997
? APPLICATION NUMBER: 60/019,053
? FILING DATE: 16-MAY-1996
? APPLICATION NUMBER: 08/160,604
? FILING DATE: 30-NOV-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Pabst, Patrea L.
? REGISTRATION NUMBER: 31,284
? REFERENCE/DOCKET NUMBER: OMRF161
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (404)873-8795
? TELEFAX: (404)873-8795
? INFORMATION FOR SEQ ID NO: 19:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 12 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? SEQUENCE DESCRIPTION: SEQ ID NO: 19
US-10-012-756-19

Query Match      26.3%; Score 26; DB 9; Length 12;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 RMRGR 12
DB 7 RRGRR 12

Search completed: March 14, 2003, 16:10:58
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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

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(without alignments)  
78.805 Million cell updates/sec

Title: US-09-674-913a-1  
Perfect score: 99  
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Scoring table: BLOSUM62  
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Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1520

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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3	30	30.3	23	1	PAP1_SPOEX
4	30	30.3	23	1	PAP2_SPOEX
5	30	30.3	23	1	PAP3_SPOEX
6	29	29.3	23	1	PAP1_HELYI
7	29	29.3	23	1	PAP2_HELYI
8	27	27.3	14	1	ADF_TENMO
9	25	25.3	24	1	DNM1_STRAG
10	24	24.2	15	1	DCNM_PSECH
11	24	24.2	25	1	DNM1_MYCCA
12	23	23.2	20	1	KORA_METTM
13	22	22.2	12	1	H2AX_ONCMY
14	22	22.2	22	1	TIH1_SPTOL
15	22	22.2	25	1	G3P2_JACOR
16	22	22.2	25	1	METE_GANAL
17	21	21.2	18	1	IBP4_PIG
18	21	21.2	16	1	MLB_SCYCA
19	21	21.2	20	1	PORC_METTM
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24	20	20.2	17	1	PKK5_PBRAM
25	20	20.2	19	1	TX3_PHONI
26	20	20.2	20	1	AROD_AMEME
27	20	20.2	20	1	LEC1_ARTIN
28	20	20.2	20	1	SAMP_PLEPL
29	20	20.2	21	1	LEC2_ARTIN
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33	19	19.2	17	1	APID_BOMPA

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37	19	19.2	25	1	FRHB_METBA
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39	18	18.2	9	1	F1BB_PAPAN
40	18	18.2	9	1	PGIR_DIAAB
41	18	18.2	10	1	PAP1_PARMA
42	18	18.2	11	1	MLG_THERS
43	18	18.2	14	1	RS19_PROAP
44	18	18.2	20	1	CUDP_VERCH
45	18	18.2	20	1	DETS_RAT
46	18	18.2	20	1	RIPX_CUCPE
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49	18	18.2	23	1	AU44_LITRA
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51	18	18.2	25	1	CXOB_CONCT
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79	17	17.2	20	1	PSAF_MAIZE
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81	17	17.2	20	1	RECX_AZOVI
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83	17	17.2	22	1	TX1_HETFU
84	17	17.2	23	1	NEUD_LITCE
85	17	17.2	23	1	TX2_HETFU
86	17	17.2	23	1	TYPH_LACCA
87	17	17.2	24	1	BOMN_BOWVA
88	17	17.2	25	1	BLP4_BOMOR
89	17	17.2	25	1	BOTR_BOTJA
90	17	17.2	25	1	H11_WHEAT
91	17	17.2	25	1	RL36_MYCCA
92	17	17.2	25	1	RS19_ACHLA
93	17	17.2	25	1	Y194_ARCFU
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96	16	16.2	8	1	ICK2_LEUMA
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98	16	16.2	10	1	BPP8_BORIN
99	16	16.2	10	1	COXO_RAT
100	16	16.2	10	1	TPIS_NICPL
101	16	16.2	12	1	RR16_GINBI
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103	16	16.2	12	1	UH03_RAT
104	16	16.2	13	1	BRP1_BOTJA
105	16	16.2	13	1	IDHA_CANFA
106	16	16.2	14	1	NEJ2_FASHE

P72180	paracoccus
O91w5	phoenicia
P29134	thiobacilli
P80490	methanosarc
P17877	clostridium
P19344	papio anubi
P1179	diaprepes a
P1863	parachirius
P41989	theromyzon
O44160	prunus arme
P80406	verticilliu
P07448	rattus norv
P80750	cucurbita p
P50071	streptomyce
P82397	litorea aur
P82400	litorea ran
P30253	manduca sex
P58918	conus calus
O47881	elm yellows
P18691	thunnus alb
P81070	fusarium so
P30087	homo sapien
P81780	herpes simp
P41860	calliphora
P41492	sarcophaga
P09039	leucophaea
P04428	leucophaea
P36885	periplaneta
P47733	locusta mig
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P01198	camelus dro
P41493	sarcophaga
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P80616	zea mays (m
P80501	solanum tub
P61093	trichosanthe
O52782	anabena sp
P01202	equus cabal
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P81530	trichuris m
P81753	leucophaea
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P82850	heterometru
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P19663	lactobacilli
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P29224	achetepiasm
O30045	archaeoglob
P21227	pisum sativ
P25140	bacillius ii
P21141	leucophaea
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P80426	rattus norv
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108	16	16.2	14	1	SAP2_ARBP	P11760 arabacia pun	181	15	15.2	21	1	NDK_CANAL	Q9u66 candida alb
109	16	16.2	15	1	ODP3_SOLTU	P81420 solanum tub	182	15	15.2	21	1	NRLA_ACISP	P33036 acinetobact
110	16	16.2	16	1	MLB_SOUTAC	P01207 squalus aca	183	15	15.2	21	1	PEDE_HYDAT	P80577 hydra atten
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112	16	16.2	17	1	AU32_LITRA	P82395 litorea ran	185	15	15.2	21	1	TRYE_PROAT	P35051 protopterus
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114	16	16.2	17	1	RM35_YEAST	P36530 saccharomyc	187	15	15.2	23	1	COX2_ONCMY	P80333 oncorhynch
115	16	16.2	17	1	TL09_SPIOL	P82671 splinacia ol	188	15	15.2	23	1	NIPD_ANASL	P33177 anapaena sp
116	16	16.2	17	1	VESP_VESMC	P57672 vesputia mac	189	15	15.2	23	1	PAP2_MANSE	P30254 manduca sex
117	16	16.2	18	1	GOME_ACAGO	P82358 acanthoscur	190	15	15.2	23	1	RL18_HALVO	P50563 natobacteri
118	16	16.2	19	1	FIBB_CERNI	P14447 cervus nipp	191	15	15.2	23	1	VG22_BPT2	P21596 bacterioph
119	16	16.2	19	1	FIBB_HORSE	P14471 equus cabal	192	15	15.2	24	1	12KD_MYCSM	P80438 mycobacteri
120	16	16.2	20	1	CISY_STRHY	P20903 streptomyce	193	15	15.2	24	1	CORC_SHEEP	Q9t30 ovis aries
121	16	16.2	20	1	FIBR_PACLE	P81070 pacifastacu	194	15	15.2	24	1	CORC_CANFA	P28490 canis famli
122	16	16.2	20	1	FRE3_LITIN	P56249 litorea inf	195	15	15.2	24	1	FED3_AMEYE	P80707 amocilatops
123	16	16.2	20	1	MCRG_METTE	P22950 methanosarc	196	15	15.2	24	1	IR31_HAEIN	P35756 haemophilus
124	16	16.2	20	1	PURK_RROSH	Q53121 rhodobacter	197	15	15.2	24	1	PSBR_WHEAT	P12358 triticum ae
125	16	16.2	20	1	SCB1_CANFA	P99507 canis famli	198	15	15.2	25	1	AMP3_MELGA	P80393 melagrifis g
126	16	16.2	21	1	ACE_BOVIN	P21532 corynebacte	199	15	15.2	25	1	H2B1_ECHES	P13381 echinus esc
127	16	16.2	22	1	LPRM_CORDI	P12820 bos taurus	200	15	15.2	25	1	LPCP_YEAST	P08521 saccharomyc
128	16	16.2	22	1	LANM_STRMU	P80666 streptococc	201	15	15.2	25	1	RL41_ARATH	P35015 arabidopsis
129	16	16.2	22	1	NUEM_SOLTU	P80765 solanum tub	202	15	15.2	25	1	RL41_HUMAN	P28751 homo sapien
130	16	16.2	22	1	PSP2_SOLTU	P80730 solanum tub	203	15	15.2	25	1	RL41_QUESU	Q82713 quercus sub
131	16	16.2	22	1	PSP2_PHYPA	P80661 physcomitre	204	15	14.6	22	1	UKA2_HUMAN	P31144 homo sapien
132	16	16.2	23	1	PS3_PSPBP	P83190 pseudis par	205	14.5	14.6	22	1	FUC1_RAT	P80347 rattus norv
133	16	16.2	23	1	VG22_BPT6	P21597 bacterioph	206	14	14.1	7	1	DCML_PSECH	P19916 pseudomonas
134	16	16.2	24	1	DHAG_COMTE	P80705 commomonas t	207	14	14.1	7	1	UN06_PINPS	P81657 pinus pinas
135	16	16.2	24	1	FIRB_CANFA	P12800 canis famli	208	14	14.1	9	1	PPK3_PERAM	P82618 periplaneta
136	16	16.2	24	1	HPR4_RABIT	P13571 oryctolagus	209	14	14.1	9	1	LIT0_LITAU	P08945 litorea aur
137	16	16.2	24	1	RS13_THETH	P80377 thermus the	210	14	14.1	9	1	LITR_PHYRO	P08946 phyllomedus
138	16	16.2	24	1	RS19_PHYS2	Q06096 phytoplasma	211	14	14.1	10	1	GLEM_HUMAN	P02728 homo sapien
139	16	16.2	25	1	COX1_PARVE	Q00502 paracoccus	212	14	14.1	10	1	GON2_CHEPR	P80678 cheiliosoma
140	16	16.2	25	1	COX6_NEUCR	Q01359 neurospora	213	14	14.1	10	1	GON3_ONCKE	P20367 oncorhynch
141	16	16.2	25	1	CXOB_CONMA	P05485 conus magus	214	14	14.1	10	1	GONL_SQUAC	P27429 squalus aca
142	16	16.2	25	1	RL41_SOYEN	Q49324 glycine max	215	14	14.1	10	1	GRP_RANRI	P23260 rana ridibu
143	15.5	15.7	18	1	CPAX_BOVIN	P22779 bos taurus	216	14	14.1	10	1	SPI_HALRO	Q10997 halocynthia
144	15.5	15.7	22	1	FUC2_RAT	P80348 rattus norv	217	14	14.1	10	1	UPA5_HUMAN	P30091 homo sapien
145	15.5	15.7	25	1	CP12_SOLTU	P24744 solanum tub	218	14	14.1	11	1	COR2_PERAM	P1496 periplaneta
146	15	15.2	3	1	GRMW_HUMAN	P01157 homo sapien	219	14	14.1	11	1	MORN_HUMAN	P01163 homo sapien
147	15	15.2	10	1	COXK_ONCMY	P80332 oncorhynch	220	14	14.1	11	1	RANC_RANPI	P08951 rana pipien
148	15	15.2	10	1	COXO_THUOB	P80982 thunnus obe	221	14	14.1	12	1	OPS3_DROVI	P17645 drosophi
149	15	15.2	11	1	TKND_RANRI	P29207 rana ridibu	222	14	14.1	12	1	SOIS_BACSU	P80863 bacillus su
150	15	15.2	11	1	TKND_RANCA	P22691 rana catesb	223	14	14.1	12	1	UR2_POLSP	P81022 polyodon sp
151	15	15.2	12	1	RS19_CLEPE	Q46490 clover yell	224	14	14.1	13	1	BOML_PSEGU	P42991 pseudophryn
152	15	15.2	12	1	TA10_TREME	P01371 tremella me	225	14	14.1	13	1	ITB5_BOVIN	P80747 bos taurus
153	15	15.2	12	1	VI4K_MSSV	P82006 white spot	226	14	14.1	13	1	SAZ2_ONCMY	P82238 oncorhynch
154	15	15.2	13	1	ORCK_ORCLI	P37086 orconectes	227	14	14.1	13	1	SAZB_ONCMY	P82239 oncorhynch
155	15	15.2	14	1	LPW_CITFR	P03056 citrobacter	228	14	14.1	14	1	ALYR_ALYOB	P08944 alytes obst
156	15	15.2	14	1	LPW_ECOLI	P03053 escherichia	229	14	14.1	14	1	FIBR_HORSE	P14452 equus cabal
157	15	15.2	14	1	LPW_SALTU	P03054 salmonella	230	14	14.1	14	1	MCRZ_METTM	P58816 methanobact
158	15	15.2	14	1	RS19_CLOPE	Q46228 clover prol	231	14	14.1	14	1	MY14_EISFO	P46979 eisenia foe
159	15	15.2	14	1	RS19_LOMBP	Q48878 loofah witc	232	14	14.1	14	1	MY14_PHEVI	P46980 pheretima v
160	15	15.2	15	1	CYSK_CLOPA	P81340 clostridium	233	14	14.1	14	1	TAT1_HV1W2	P12509 human immun
161	15	15.2	15	1	EF1A_MITCR	P81266 mlticoplitis	234	14	14.1	14	1	TAT1_HV1Z8	P12511 human immun
162	15	15.2	15	1	MCA2_RHOOP	P56870 rhodococcus	235	14	14.1	14	1	UN46_CLOPA	P81652 clostridium
163	15	15.2	15	1	SALI_ONCMY	P81369 oncorhynch	236	14	14.1	15	1	ALB2_TRASC	P81189 tracheuys s
164	15	15.2	15	1	TERM_BPM2	P19897 bacterioph	237	14	14.1	15	1	ESTR_MANSE	P19855 manduca sex
165	15	15.2	16	1	DBH3_RHILE	P80605 rhizobium l	238	14	14.1	15	1	EGF1_CANFA	P18651 canis famli
166	15	15.2	16	1	PIRA_MUSVI	P14458 mustela vis	239	14	14.1	15	1	MAOX_CHICK	Q92060 gallus gall
167	15	15.2	16	1	PPAC_BACME	P56948 bacillus vis	240	14	14.1	16	1	FIBA_ODOHE	P14459 odocoileus
168	15	15.2	17	1	B29K_PORGI	P81784 porphyromon	241	14	14.1	16	1	FOR1_MYRGU	P81438 myrmecia gu
169	15	15.2	17	1	BOLA_MEGPE	P07495 megabombus	242	14	14.1	16	1	SALI_ONCMY	P82240 oncorhynch
170	15	15.2	18	1	NPA_BOVIN	P15506 bos taurus	243	14	14.1	17	1	EFG_THEAO	Q01697 thermus aqu
171	15	15.2	18	1	PH1_PERAM	P82694 periplaneta	244	14	14.1	17	1	PH4_PERAM	P82697 periplaneta
172	15	15.2	18	1	PAZS_PROVU	P20032 proteus vul	245	14	14.1	17	1	PSBL_STYNU	P12241 synecchococc
173	15	15.2	19	1	PAZS_HUMAN	P24606 homo sapien	246	14	14.1	17	1	RANR_RANRU	P80852 rana rugosa
174	15	15.2	19	1	RS19_SPEIC	Q31159 spiroplasma	247	14	14.1	17	1	UP36_UPEMT	P0236 uperoleia m
175	15	15.2	20	1	CAT4_FASHE	P80528 fasciola he	248	14	14.1	18	1	AGI_EUPMA	P33389 euphorbia m
176	15	15.2	20	1	DNAK_CLOPA	P81341 clostridium	249	14	14.1	19	1	ADC_CLOPA	P81335 clostridium
177	15	15.2	20	1	DNAK_THIFE	P29133 thibacillu	250	14	14.1	19	1	BRKM_BOMAX	P83055 bombina max
178	15	15.2	20	1	OXLA_CEOAT	P56742 crocalus at	251	14	14.1	19	1	FIBA_CEREL	P14446 cervus elap
179	15	15.2	20	1	PSBM_WHEAT	P55967 triticum ae	252	14	14.1	19	1	FIBA_SHEEP	P14451 ovis aries

253	14	14.1	19	1	LCRP_PETMA	010996	petromyzon	326	13	13.1	10	1	GONI_CLUPA	P81749	clupea pall
254	14	14.1	19	1	PCG7_PACGO	P82420	pachycondyl	327	13	13.1	10	1	GONI_PETMA	P04378	petromyzon
255	14	14.1	20	1	ALAT_PIG	P13191	sus scrofa	328	13	13.1	10	1	GONI_CHICK	P37043	gallus gall
256	14	14.1	20	1	COXB_THUOB	P80974	thunnus obe	329	13	13.1	10	1	GONI_PETMA	P30948	petromyzon
257	14	14.1	20	1	EFVU_MYCSI	P81407	mycoplasma	330	13	13.1	10	1	HTE_NAUCI	P10939	nauphoeta c
258	14	14.1	20	1	FLAW_AZOVI	P52964	azotobacter	331	13	13.1	10	1	HTE_TABAT	P14596	tabanus atr
259	14	14.1	20	1	HELT_HELUO	P46693	heloderma h	332	13	13.1	10	1	PNEU_HUMAN	P22103	homo sapien
260	14	14.1	20	1	ITRA_ALBUO	P24625	albizzia ju	333	13	13.1	10	1	PNEU_RAT	P21996	rattus norv
261	14	14.1	20	1	LEC3_ARTIN	P18673	artocarpus	334	13	13.1	10	1	SLAP_BACNG	P49325	rattus norv
262	14	14.1	20	1	PSAL_SYNUZ	P25937	synechococ	335	13	13.1	10	1	VEG6_BACSU	P80699	bacillus su
263	14	14.1	20	1	SB18_MAIZE	P82667	zea mays (m	336	13	13.1	11	1	ANCT_CRIGE	P09037	crinia geor
264	14	14.1	20	1	VSP1_AGRBI	P33588	agkistrodon	337	13	13.1	11	1	BPP_AGRHP	P04562	agkistrodon
265	14	14.1	20	1	YOA8_KLEAE	P56506	klebsiella	338	13	13.1	11	1	BRK_MEGFL	P12797	megascolla
266	14	14.1	21	1	FIIBB_BUBBU	P14467	bubalus bub	339	13	13.1	11	1	COXA_CANFA	P99501	canis famli
267	14	14.1	21	1	REV_HV2D2	P15830	human immun	340	13	13.1	11	1	LAD1_ONCMY	P81018	oncorhynch
268	14	14.1	21	1	SYA_RAT	P50475	rattus norv	341	13	13.1	11	1	LPM_THETH	P05624	thermus the
269	14	14.1	21	1	YD90_HAEIN	P45194	haemophilus	342	13	13.1	11	1	TKNA_ONCMY	P28499	oncorhynch
270	14	14.1	22	1	ANFC_CHICK	P21805	gallus gall	343	13	13.1	11	1	TKNA_SCYCA	P41333	scyllorhinu
271	14	14.1	22	1	CR34_LITCE	P56241	littoria cae	344	13	13.1	12	1	PORD_METTM	P80903	methanobact
272	14	14.1	22	1	RL41_METJA	P54025	methanococ	345	13	13.1	13	1	BRK_PARID	P42717	parapolybia
273	14	14.1	23	1	AL15_HORSE	P82616	equus cabal	346	13	13.1	13	1	CXA2_CONGE	P01520	conus geogr
274	14	14.1	23	1	AU42_LITRA	P82398	littoria ran	347	13	13.1	13	1	CXA4_CONST	P28878	conus stria
275	14	14.1	23	1	AU43_LITAU	P82399	littoria aur	348	13	13.1	13	1	FIBA_CAVPO	P14445	cavia porce
276	14	14.1	23	1	GRP_ONCMY	O9ps30	oncorhynch	349	13	13.1	13	1	TEML_RANTE	P56917	rana tempor
277	14	14.1	23	1	MDH_THREXL	P33163	thermoleoph	350	13	13.1	13	1	UN12_CLOPA	P81353	clostridium
278	14	14.1	23	1	RT21_BOVIN	P82920	bos taurus	351	13	13.1	13	1	CXA1_CONCN	P56973	conus conso
279	14	14.1	24	1	TL17_SPIOI	P81778	splachia ol	352	13	13.1	14	1	CXA1_CONMA	P01521	conus magus
280	14	14.1	24	1	CCAA_STRTI	P80436	streptomyce	353	13	13.1	14	1	FIIBB_MANLE	P14474	mandrillus
281	14	14.1	24	1	CT31_LITCI	P81851	littoria cit	354	13	13.1	14	1	IFP2_RAT	P81795	rattus norv
282	14	14.1	24	1	DMS6_PHYBI	P81490	phyllomedus	355	13	13.1	14	1	UC18_MAIZE	P80624	zea mays (m
283	14	14.1	24	1	IMPT_GALME	P82176	galleria me	356	13	13.1	14	1	UN07_CLOPA	P81352	clostridium
284	14	14.1	24	1	PCL2_PACGO	P82421	pachycondyl	357	13	13.1	15	1	COXJ_THUOB	P80697	thunnus obe
285	14	14.1	24	1	PC12_PACGO	P82422	pachycondyl	358	13	13.1	15	1	CX1B_CONBE	P58624	conus betul
286	14	14.1	24	1	PSAH_CUCISA	P42050	cucumis sat	359	13	13.1	15	1	FIBA_ANAPL	P12801	anus platyr
287	14	14.1	24	1	REL1_ECOLI	P56980	escherichia	360	13	13.1	15	1	GLN2_PINPS	P81107	pinus pinas
288	14	14.1	24	1	REL2_ECOLI	O9wt7	escherichia	361	13	13.1	15	1	KLOM_LUMTE	P11918	lumbircus t
289	14	14.1	24	1	TX6B_PHYSE	P58912	phyllodiscu	362	13	13.1	15	1	PH2_PERAM	P82695	trimeresuru
290	14	14.1	24	1	VFB_BPD10	P13771	bacterioph	363	13	13.1	15	1	PLAS_MICAE	P10625	microcystis
291	14	14.1	24	1	Y3KD_NEUCR	P22702	neurospora	364	13	13.1	15	1	TA1_TREBR	P34070	tremella br
292	14	14.1	25	1	ACP_ACICPA	P80916	actinetobact	365	13	13.1	15	1	UC16_MAIZE	P80622	zea mays (m
293	14	14.1	25	1	COXO_ONCMY	P80937	alcaligenes	366	13	13.1	15	1	UC19_MAIZE	P80625	zea mays (m
294	14	14.1	25	1	CR22_LITGI	P56234	littoria gil	367	13	13.1	15	1	UN01_PINPS	P81106	pinus pinas
295	14	14.1	25	1	CR25_LITGI	P56237	littoria gil	368	13	13.1	15	1	UN04_PINPS	P81673	pinus pinas
296	14	14.1	25	1	GLMK_PREBR	P82680	prevotella	369	13	13.1	15	1	UN07_CLOPA	P41839	calliphora
297	14	14.1	25	1	GRP_SCYCA	P09472	scyllorhinu	370	13	13.1	16	1	ALL1_CALVO	P24134	streptomyce
298	14	14.1	25	1	IPYR_PSEAN	P80898	pseudonabae	371	13	13.1	16	1	FENR_STRGR	P14456	meles meles
299	14	14.1	25	1	NEUU_CHICK	P34963	gallus gall	372	13	13.1	16	1	FIBA_MELE	P14461	oryctolagus
300	14	14.1	25	1	RS11_THETH	P80376	thermus the	373	13	13.1	16	1	PA21_TRIST	P82892	trimeresuru
301	14	14.1	25	1	RT06_BOVIN	P82931	bos taurus	374	13	13.1	16	1	UVSX_BPT6	O06728	bacterioph
302	14	14.1	25	1	VGJ_BP64	P03632	bacterioph	375	13	13.1	16	1	AL1S_MYCPH	P81528	mycobacteri
303	14	14.1	25	1	NEF_HV1J3	P12480	human immun	376	13	13.1	17	1	BOLS_MEGPE	P07496	megablobus
304	13.5	13.6	17	1	LEC2_MACPO	P18676	macclura pom	377	13	13.1	17	1	PH3_PERAM	P30800	ocotopus vul
305	13.5	13.6	20	1	FAR2_ASCSU	P18990	ascaris su	378	13	13.1	17	1	A2M_OCTYU	P80582	mycobacteri
306	13	13.1	7	1	UF03_ACHPU	P38641	mus musculu	379	13	13.1	18	1	SODM_MYCHA	O02005	rhodospendo
307	13	13.1	7	1	WMA3_ACHPU	P35921	echatina fu	380	13	13.1	18	1	YAA5_RHOPA	002022	lactococcus
308	13	13.1	8	1	AAH_TABAT	P14595	tabanus atr	381	13	13.1	18	1	YPE4_LACLC	P44022	lactococcus
309	13	13.1	8	1	LCK5_STEUA	P19987	leucophaea	382	13	13.1	18	1	FIBA_BUBBU	P14442	bubalus bub
310	13	13.1	8	1	LPMS_STEUA	P23211	staphylococ	383	13	13.1	19	1	HBB2_UROHA	P18992	urosaestylx h
311	13	13.1	8	1	RPCH_PANMO	P08939	pandalus bo	384	13	13.1	19	1	H170_RAT	P21794	rattus norv
312	13	13.1	8	1	UF06_MOUSE	P38644	mus musculu	385	13	13.1	19	1	HMD_METMO	P32441	m coenzyme
313	13	13.1	8	1	UFPA_HUMAN	P30096	homo sapien	386	13	13.1	19	1	TP1S_CLOPA	P82031	uperoleia l
314	13	13.1	8	1	FARP_CALSI	P38495	macaca fusc	387	13	13.1	19	1	UP25_UPEIN	P82039	uperoleia m
315	13	13.1	9	1	FIIBB_MACFU	P19343	macaca fusc	388	13	13.1	19	1	UP27_UPEMJ	P82040	uperoleia m
316	13	13.1	9	1	FIIBB_PAPHA	P19343	papio hamad	389	13	13.1	19	1	ABP_PIG	O9trc7	sus scrofa
317	13	13.1	9	1	SAMP_MUSCA	P19095	muscielus ca	390	13	13.1	20	1	BULB_NARPS	P34153	chironocete
318	13	13.1	9	1	UTAH_HUMAN	P31934	homo sapien	391	13	13.1	20	1	COG1_CHTOP	P20731	parallithode
319	13	13.1	9	1	UPAG_HUMAN	P30092	homo sapien	392	13	13.1	20	1	COG2_PARCM	P34154	chironocete
320	13	13.1	10	1	AMPN_HELAM	P31351	hellioverpa	393	13	13.1	20	1	COG3_CHTOP	P34155	chironocete
321	13	13.1	10	1	BPP_VIPAS	O9prz1	oncorhynch	394	13	13.1	20	1	COGA_PARCM	P20732	parallithode
322	13	13.1	10	1	BRK_ONCMY	P37041	alligator m	395	13	13.1	20	1			
323	13	13.1	10	1	GONI_ALIMI	P80677	chelyosoma	396	13	13.1	20	1			
324	13	13.1	10	1				397	13	13.1	20	1			
325	13	13.1	10	1	GONI_CHEPR			398	13	13.1	20	1			

399	13	13.1	20	1	COGB_PARCM	P20733	parallithode	472	12	12.1	9	1	OXYT_EISFO	P42998	eisenia foe
400	13	13.1	20	1	COXA_THUOB	P80972	thunnus obe	473	12	12.1	9	1	OXYT_OCTVU	P80027	octopus vul
401	13	13.1	20	1	COXN_THUOB	P80960	thunnus obe	474	12	12.1	9	1	OXYT_RABIT	P32878	oryctolagus
402	13	13.1	20	1	FIBB_ELEMA	P14558	elephas max	475	12	12.1	9	1	OXYT_RABIT	P42994	raja clavat
403	13	13.1	20	1	KORC_METTM	P80966	methanobact	476	12	12.1	9	1	OXYV_SQUAC	P43000	squalus aca
404	13	13.1	20	1	LEC3_MACPO	P18677	maciura pom	477	12	12.1	10	1	ANGT_BOVIN	P01017	bos taurus
405	13	13.1	20	1	LEC3_MACPO	P05658	bacillus st	478	12	12.1	10	1	COXM_RAT	P80413	rattus norv
406	13	13.1	20	1	LEPR_BACST	P23053	bacillus su	479	12	12.1	10	1	COXM_RAT	P11755	locusta mig
407	13	13.1	20	1	LYC_FELCA	P37155	felis silve	480	12	12.1	11	1	CEPI_ACHFU	P41488	locusta mig
408	13	13.1	20	1	NEUA_RAT	P29188	rattus norv	481	12	12.1	11	1	CEPI_ACHFU	P23790	achaelina fu
409	13	13.1	20	1	RLC1_HALMA	P12740	haloarcula	482	12	12.1	11	1	TKNA_RANCA	P83328	oncorhynch
410	13	13.1	20	1	RLC1_HALMA	P05511	sus scrofa	483	12	12.1	11	1	TKNA_RANCA	P22668	rana catesb
411	13	13.1	20	1	TPX_CLOFA	P81361	clostridium	484	12	12.1	12	1	PSP3_PHYPA	P80662	physcomile
412	13	13.1	20	1	VSP1_TRIOR	P20005	trimeresur	485	12	12.1	12	1	TKN_KASSE	P88611	kassina sen
413	13	13.1	21	1	CSP1_STRIK	P16522	streptococc	486	12	12.1	12	1	V23K_WSSV	P82005	white spot
414	13	13.1	21	1	FIBB_BISBO	P14466	bison bonas	487	12	12.1	13	1	AU11_LITRA	P82366	litoria ran
415	13	13.1	21	1	GIG1_SPTOL	P55246	spinnacia ol	488	12	12.1	13	1	AU12_LITRA	P82097	litoria ran
416	13	13.1	21	1	GRX_BUNCN	P58305	bunodosoma	489	12	12.1	13	1	EI22_LITRU	P82098	litoria rub
417	13	13.1	21	1	LEC1_MACPO	P18675	maciura pom	490	12	12.1	13	1	NP2_LYNST	P80179	lymaea sta
418	13	13.1	21	1	MCT3_MOUSE	P21843	mus musculu	491	12	12.1	13	1	NP5_LYNST	P80182	lymaea sta
419	13	13.1	21	1	RL5_HALME	P50561	halobacteri	492	12	12.1	13	1	PSBP_PLNPS	P81668	pinus pinas
420	13	13.1	21	1	THAN_PODMA	P50557	halobacteri	493	12	12.1	13	1	TA13_TREME	P01370	tremella me
421	13	13.1	21	1	YELA_METVO	P42017	methanococc	494	12	12.1	13	1	UN41_CLOPA	P40928	homo sapien
422	13	13.1	22	1	AOFA_MOUSE	P06413	mus musculu	495	12	12.1	14	1	ANGT_HORSE	P01016	equus cabal
423	13	13.1	22	1	CYTB_THETS	P81064	theromyzon	496	12	12.1	14	1	DHSL_ANACE	P17874	anabrena cy
424	13	13.1	22	1	PAZ_DABRU	P18999	dabola russ	497	12	12.1	14	1	HY1A_PIG	P01155	sus scrofa
425	13	13.1	22	1	RL18_HALME	P50561	halobacteri	498	12	12.1	14	1	MAST_PARID	P42716	parapolybia
426	13	13.1	22	1	RL5_HALVO	P50559	halobacteri	499	12	12.1	14	1	MAST_VESLE	P01514	vespula lew
427	13	13.1	22	1	UC07_MAIZE	P80613	zea mays (m	500	12	12.1	15	1	CDN2_LITGI	P56247	litoria gyl
428	13	13.1	22	1	UVSX_BPT2	P06727	bacterioph	501	12	12.1	15	1	CHX1_CONGE	P01519	conus geogr
429	13	13.1	22	1	YORK_CABEL	P09290	caenorhabdi	502	12	12.1	15	1	ESTR_SCHGA	P21241	schizaphis
430	13	13.1	23	1	CLVB_STYCL	P80711	stelyria clav	503	12	12.1	15	1	NUO3_SOLTU	P80263	solanum tub
431	13	13.1	23	1	CR42_LITCE	P56242	litoria cae	504	12	12.1	15	1	UC17_MAIZE	P01159	rattus norv
432	13	13.1	23	1	POQA_KLEPN	P27503	klepsidella	505	12	12.1	15	1	BAIL_EUBSP	P80623	zea mays (m
433	13	13.1	23	1	PS4_PSEPD	P83191	pseudis par	506	12	12.1	16	1	CAT9_FASHE	P32371	eubacterium
434	13	13.1	23	1	RL5_HALHA	P50566	halobacteri	507	12	12.1	16	1	DHE2_THOUT	P80553	fasciola he
435	13	13.1	23	1	UHA4_HUMAN	P49289	homo sapien	508	12	12.1	16	1	FIBA_FOUAS	P20016	thunnus thy
436	13	13.1	24	1	ACHA_ELEEL	P09688	electrophor	509	12	12.1	16	1	FIBA_HYULA	P14449	equus asinu
437	13	13.1	24	1	CAMT_PINPS	P81081	pinus pinas	510	12	12.1	16	1	FIBA_MACFU	P14453	hylobates l
438	13	13.1	24	1	CH60_ACTICA	P81874	actinetobact	511	12	12.1	16	1	OTRC_AREMA	P112803	macaca fusc
439	13	13.1	24	1	DLAA_AMYME	P80413	amycolalops	512	12	12.1	16	1	ODPA_SOLTU	P11917	arenicola m
440	13	13.1	24	1	ODDP_BOVIN	P11966	bos taurus	513	12	12.1	16	1	RBL_CAPAN	P82063	solanum tub
441	13	13.1	24	1	PS1_PSEPD	P83188	pseudis par	514	12	12.1	16	1	RBL_CUCSA	P27064	cucumis sat
442	13	13.1	24	1	PS2_PSEPD	P83189	pseudis par	515	12	12.1	16	1	BOL1_MEGPE	P27067	vigna sinen
443	13	13.1	24	1	RAN_XENLA	P52301	xenopus lae	516	12	12.1	17	1	BOL2_MEGPE	P10521	megabombus
444	13	13.1	24	1	VGJ_BPAL3	P08766	bacterioph	517	12	12.1	17	1	UC21_KLEAE	P07494	megabombus
445	13	13.1	25	1	ACP_ERYLO	P80919	erythrobact	518	12	12.1	17	1	UP34_UPEMJ	P82041	upetroleia t
446	13	13.1	25	1	DNAR_ACTICA	P81875	actinetobact	519	12	12.1	17	1	AHD2_TETPY	P35430	tetrahymena
447	13	13.1	25	1	FIB3_TREHY	P80161	therponema h	520	12	12.1	18	1	FMFL_ECOLI	P20660	escherichia
448	13	13.1	25	1	K6P2_THETH	P21778	thermus the	521	12	12.1	18	1	UC21_KLEAE	P81098	heliannthus
449	13	13.1	25	1	NCP_PIG	P80552	sus scrofa	522	12	12.1	18	1	TOP1_KLEAE	P46155	klebsiella
450	13	13.1	25	1	PRLA_ACHLY	P78569	agarcia bi	523	12	12.1	18	1	UP34_UPEMJ	P80532	fasciola he
451	13	13.1	25	1	RL41_AGABI	P09710	schizosacch	524	12	12.1	18	1	FMFL_ECOLI	P58811	conus tulip
452	13	13.1	25	1	RL41_AGABI	P09684	gadus morhu	525	12	12.1	18	1	MDH_BREDE	P14440	antilocapra
453	13	13.1	25	1	RL41_AGABI	P08497	bacillus su	526	12	12.1	18	1	MDH_BREDE	P33936	escherichia
454	13	13.1	25	1	UBLI_YEAST	P09839	mus musculu	527	12	12.1	19	1	MDH_SHEON	P80542	brevundimon
455	13	13.1	25	1	VIP_GADMO	P82065	litoria rub	528	12	12.1	19	1	MDH_SHEON	P82177	shewanella
456	13	13.1	25	1	UBLI_BOVIN	P23356	bos taurus	529	12	12.1	19	1	MDH_SHEON	P81329	trichinella
457	13	13.1	25	1	VIP_GADMO	P09839	mus musculu	530	12	12.1	19	1	MDH_SHEON	P24365	streptococc
458	12.5	12.6	24	1	UPO1_MOUSE	P82065	litoria rub	531	12	12.1	19	1	MDH_SHEON	P56610	titicus bali
459	12	12.1	5	1	TY51_LITRU	P56577	rattus norv	532	12	12.1	20	1	MDH_SHEON	P80085	spinnacia ol
460	12	12.1	7	1	UHI1_RAT	P82152	cydia pomon	533	12	12.1	20	1	MDH_SHEON	P19633	rattus norv
461	12	12.1	8	1	ALL1_CYPDPO	P82152	cydia pomon	534	12	12.1	20	1	MDH_SHEON	P20734	parallithode
462	12	12.1	8	1	UHI1_RAT	P82152	cydia pomon	535	12	12.1	20	1	MDH_SHEON		
463	12	12.1	9	1	UHI1_RAT	P82152	cydia pomon	536	12	12.1	20	1	MDH_SHEON		
464	12	12.1	9	1	UHI1_RAT	P82152	cydia pomon	537	12	12.1	20	1	MDH_SHEON		
465	12	12.1	9	1	UHI1_RAT	P82152	cydia pomon	538	12	12.1	20	1	MDH_SHEON		
466	12	12.1	9	1	UHI1_RAT	P82152	cydia pomon	539	12	12.1	20	1	MDH_SHEON		
467	12	12.1	9	1	UHI1_RAT	P82152	cydia pomon	540	12	12.1	20	1	MDH_SHEON		
468	12	12.1	9	1	UHI1_RAT	P82152	cydia pomon	541	12	12.1	20	1	MDH_SHEON		
469	12	12.1	9	1	UHI1_RAT	P82152	cydia pomon	542	12	12.1	20	1	MDH_SHEON		
470	12	12.1	9	1	UHI1_RAT	P82152	cydia pomon	543	12	12.1	20	1	MDH_SHEON		
471	12	12.1	9	1	UHI1_RAT	P82152	cydia pomon	544	12	12.1	20	1	MDH_SHEON		

545	12	12.1	20	1	COX2_OXCMY	P80335 oncorhynch	618	11	11.1	10	1	AH3_PRUSE	P29261 prunus sero
546	12	12.1	20	1	CS21_STRPR	P30866 spiliocia ol	619	11	11.1	10	1	AKH3_LOCM1	P81626 locusta mig
547	12	12.1	20	1	DNK2_MYCAB	P80462 mycobacteri	620	11	11.1	10	1	COXH_OXCMY	P80331 oncorhynch
548	12	12.1	20	1	LECB_TRIRIO	P80231 liris holian	621	11	11.1	10	1	GAU2_HUMAN	P01358 homo sapien
549	12	12.1	20	1	PER_BACCE	P80375 bacillus ce	622	11	11.1	10	1	SP34_DICMU	P81545 dictyostel
550	12	12.1	20	1	TEMA_ACTTE	P30833 actinia ten	623	11	11.1	10	1	SYR_CANUP	Q4646 campylobact
551	12	12.1	20	1	TRR8_ECOLI	P33789 escherichia	624	11	11.1	10	1	TKNB_CHICK	P4651 gallicus gall
552	12	12.1	20	1	TRYL_ECOLI	P33789 escherichia	625	11	11.1	10	1	TKU2_UREUN	P40752 urechis uni
553	12	12.1	20	1	TRR8_ECOLI	P33789 escherichia	626	11	11.1	10	1	TRP5_LEUMA	P81737 leucophaea
554	12	12.1	20	1	VR90_BOREA	P80420 streptomyce	627	11	11.1	10	1	TRP7_LEUMA	P81739 leucophaea
555	12	12.1	20	1	ATPB_PHYRA	P80568 physconitre	628	11	11.1	10	1	TRP8_LEUMA	P81740 leucophaea
556	12	12.1	21	1	CHIC_PEA	P31233 pisum sativ	629	11	11.1	10	1	TRP9_LEUMA	P81741 leucophaea
557	12	12.1	21	1	LPT_ECOLI	P30359 escherichia	630	11	11.1	10	1	UPA4_HUMAN	P30090 homo sapien
558	12	12.1	21	1	MDR_RHOP	P80458 rhodopseudo	631	11	11.1	10	1	UPA8_HUMAN	P30090 homo sapien
559	12	12.1	21	1	MISG_MISAN	P81474 misgurinus a	632	11	11.1	11	1	CA31_LITCI	P82089 litoria cit
560	12	12.1	21	1	PSBF_SYNUU	P12239 synchococc	633	11	11.1	11	1	CA32_LITCI	P82090 litoria cit
561	12	12.1	21	1	SP13_SOLU	P85816 solanum tub	634	11	11.1	11	1	ES1_RAT	P56571 rattus norv
562	12	12.1	22	1	CR32_LITCE	P86239 litoria cae	635	11	11.1	11	1	NUHM_CANPA	P49820 canis fami
563	12	12.1	22	1	CR33_LITCE	P86240 litoria cae	636	11	11.1	11	1	T2P1_PROVU	P31031 proteus vul
564	12	12.1	22	1	CR1_CLOPA	P81357 clostridium	637	11	11.1	11	1	TKC2_CALVO	P41518 calliphora
565	12	12.1	22	1	HS71_LEIRA	P85938 leishmania	638	11	11.1	11	1	TKN_ELEMO	P01293 elledone mos
566	12	12.1	22	1	IF2G_PIG	P20461 sus scrofa	639	11	11.1	12	1	FAR1_CALVO	P41869 calliphora
567	12	12.1	22	1	LPI_TRIMA	P24335 trimeresuru	640	11	11.1	12	1	GRAR_RANRU	P40754 rana rugosa
568	12	12.1	22	1	LPI_TRIMA	P88930 trimeresuru	641	11	11.1	12	1	LM71_LOCM1	P22395 locusta mig
569	12	12.1	22	1	LPT_CORGL	P2456 corynebacte	642	11	11.1	12	1	RFL_CONSP	P58805 conus spuri
570	12	12.1	22	1	LPT_SRRMA	O84208 serratia ma	643	11	11.1	12	1	TKN2_KASMA	P08614 kassina mac
571	12	12.1	22	1	MOT1_CANRA	P19863 canis fami	644	11	11.1	12	1	UR2A_CAPCO	P04558 catostomus
572	12	12.1	22	1	PHAI_BOVIN	P55930 bos laurus	645	11	11.1	12	1	UR2B_CITCA	P04561 cyprinus ca
573	12	12.1	23	1	CR43_LITCE	P56244 litoria cae	646	11	11.1	13	1	AH4_PRUSE	P23262 pinus sero
574	12	12.1	23	1	CKCV_CONTE	P58845 conus texti	647	11	11.1	13	1	BLAC_STRGR	P81173 streptomyc
575	12	12.1	23	1	GLNA_PHOLP	P20479 phormidium	648	11	11.1	13	1	BP37_LEUMA	P40754 rana rugosa
576	12	12.1	24	1	BRIA_RANES	P40835 rana escul	649	11	11.1	13	1	CPI_APICA	P81754 leucophaea
577	12	12.1	24	1	COXC_THUOB	P80973 thunnus obe	650	11	11.1	13	1	CRBL_ICASP	Q10998 aplysia cal
578	12	12.1	24	1	FURE_RANCA	P55736 rana catesb	651	11	11.1	13	1	ECDE_LYMDI	P17237 icaria sp.
579	12	12.1	24	1	FRE4_LITIN	P82032 litoria inf	652	11	11.1	13	1	LMAI_LOCM1	P80941 lymantria d
580	12	12.1	24	1	HEMT_LITNE	P23543 litoria ree	653	11	11.1	13	1	LEPA_PORGI	P81411 porphyromon
581	12	12.1	24	1	HS9B_RABIT	P30947 cyclocolagus	654	11	11.1	13	1	NEUT_CAVPO	P32560 pinus sero
582	12	12.1	24	1	KPKY_CLOPA	P13344 clostridium	655	11	11.1	13	1	NPI_LYMSY	P80178 lymnaea sta
583	12	12.1	24	1	LEPR_STRPR	P45440 streptomyc	656	11	11.1	13	1	PHGR_FUBOX	P57793 bacillus
584	12	12.1	24	1	PA24_TRIST	P88895 trimeresuru	657	11	11.1	13	1	PSAE_PEA	P20118 pisum sativ
585	12	12.1	24	1	PEP1_ASPNG	P55749 aspergillus	658	11	11.1	13	1	UP71_LITFW	P82050 litoria ewi
586	12	12.1	24	1	POOA_ACTCA	P25177 acinetobact	659	11	11.1	14	1	CAT2_FASHE	P80342 fasciola he
587	12	12.1	24	1	POOA_PSEEL	P56233 litoria spl	660	11	11.1	14	1	COCO_LITPO	P35586 limulus pol
588	12	12.1	25	1	CR21_LITSP	P56233 litoria cae	661	11	11.1	14	1	GLPK_STRGR	P25013 streptomyc
589	12	12.1	25	1	CR23_LITCE	P56233 litoria cae	662	11	11.1	14	1	HCVI_MESCR	Q10583 megastira c
590	12	12.1	25	1	CR24_LITCE	P80891 litoria cae	663	11	11.1	14	1	KARA_BROPL	P22442 bromelia p
591	12	12.1	25	1	GYC4_YIBFI	P80891 litoria cae	664	11	11.1	14	1	LEPR_BACLI	Q04303 bacillus ii
592	12	12.1	25	1	GBX1_MOUSE	P82976 mus muscul	665	11	11.1	14	1	MAST_POLJA	P01517 polistes ja
593	12	12.1	25	1	LE01_BIOGL	P80742 biomphalari	666	11	11.1	14	1	MAST_VESMA	P04205 vespa manda
594	12	12.1	25	1	MDH_PHEIM	P19080 phenylloact	667	11	11.1	14	1	MAST_VESXA	P01515 vespa xanth
595	12	12.1	25	1	MT_NEUCR	P02807 neurospora	668	11	11.1	14	1	SODN_STRGR	P80732 streptomyc
596	12	12.1	25	1	PAZH_HOTSC	P80963 bochrhechis	669	11	11.1	15	1	48KD_BACCE	P80173 bacillus ce
597	12	12.1	6	1	E101_LITRU	P82096 litoria rub	670	11	11.1	15	1	ACEA_ACTCA	P28467 acinetobact
598	12	12.1	7	1	E105_LITRU	P82096 litoria rub	671	11	11.1	15	1	ACT_PIPNS	P81085 pinus pinas
599	12	12.1	7	1	UC24_MAIZE	P80630 zea mays (m	672	11	11.1	15	1	AH2_PRUSE	P29260 pinus sero
600	12	12.1	7	1	UF04_MOUSE	P36642 mus muscul	673	11	11.1	15	1	ARCA_STRPS	P58827 streptococ
601	12	12.1	8	1	ALIS_CYPDO	P82156 cydia pomon	674	11	11.1	15	1	CHIL_PEA	P21225 pisum sativ
602	12	12.1	8	1	CCKN_MACEU	P30369 macrospora eu	675	11	11.1	15	1	COXI_THUOB	P80978 thunnus obe
603	12	12.1	8	1	GLUR_HUMAN	P07729 homo sapien	676	11	11.1	15	1	FTBA_SYNCA	P14463 syncerus ca
604	12	12.1	8	1	NS3_MYCTU	P81152 mycobacteri	677	11	11.1	15	1	ITRB_ALBUU	P24927 albizia ju
605	12	12.1	9	1	COXE_THUOB	P80975 thunnus obe	678	11	11.1	15	1	LECI_PSOIC	P23582 psophocarpu
606	12	12.1	9	1	DSIP_RABIT	P01158 otycolagus	679	11	11.1	15	1	LPE_ECOLI	P30357 escherichia
607	12	12.1	9	1	FAR2_CALVO	P41857 calliphora	680	11	11.1	15	1	MORA_MENTE	P22448 methanosarc
608	12	12.1	9	1	FAR3_CALVO	P41858 calliphora	681	11	11.1	15	1	MILT_ONCKE	P81037 oncorhynch
609	12	12.1	9	1	FAR4_CALVO	P41859 calliphora	682	11	11.1	15	1	MM01_RAT	P81563 rattus norv
610	12	12.1	9	1	FARA_CALVO	P41865 calliphora	683	11	11.1	15	1	NUO6_SOLJU	P80731 solanum tub
611	12	12.1	9	1	FIBB_ERIPA	P19346 erythrocebu	684	11	11.1	15	1	R13A_SPTOL	P82454 spinacia ol
612	12	12.1	9	1	FIBB_TREHY	P19347 erythrocebu	685	11	11.1	15	1	R13A_SPTOL	Q9X320 streptomyc
613	12	12.1	9	1	FLA2_TREHY	P80159 treponema h	686	11	11.1	15	1	R13A_SPTOL	P81347 clostridium
614	12	12.1	9	1	LMT3_LOCM1	P41489 locusta mig	687	11	11.1	15	1	UC01_MAIZE	P80607 zea mays (m
615	12	12.1	9	1	TRP4_LEUMA	P81736 leucophaea	688	11	11.1	15	1	UC06_MAIZE	P80619 zea mays (m
616	12	12.1	9	1	ULAK_MOUSE	P90031 mus muscul	689	11	11.1	15	1	UC13_MAIZE	P80619 zea mays (m
617	12	12.1	9	1	UPA7_HUMAN	P30093 homo sapien	690	11	11.1	15	1	UC29_MAIZE	P80635 zea mays (m

691	11	11.1	15	1	YAA3_RHOA	Q02006 rhodopseudo	764	11	11.1	20	1	VMO2_CHICK	Q9ps49 gallus gall
692	11	11.1	16	1	AH1_PROSE	P22259 prunus sero	765	11	11.1	21	1	PRX_ATTRE	P80163 attractaspis
693	11	11.1	16	1	ALRX_PSEPU	P17916 pseudomonas	766	11	11.1	21	1	CAKT_CONUT	P17684 conus tulip
694	11	11.1	16	1	CT11_LITCI	P81835 litorea cit	767	11	11.1	21	1	FIBB_ANTAM	P14461 antioctapia
695	11	11.1	16	1	CT12_LITCI	P81840 litorea cit	768	11	11.1	21	1	FIBB_SYNCA	P14481 synecrus ca
696	11	11.1	16	1	CT13_LITCI	P81846 litorea cit	769	11	11.1	21	1	MDH_BURCE	P80537 burholderi
697	11	11.1	16	1	CXAI_CONEP	P56638 conus episc	770	11	11.1	21	1	MDH_PSEIN	P80568 pseudomonas
698	11	11.1	16	1	CXAA_CONEP	P50984 conus penna	771	11	11.1	21	1	MD11_LITGE	P82066 litorea gen
699	11	11.1	16	1	FIRA_TAPTE	P14536 tapirus ter	772	11	11.1	21	1	ODP2_SOLTU	P81421 solanum tub
700	11	11.1	16	1	FOR2_MYRGU	P81437 myrmecia gu	773	11	11.1	21	1	OMP1_HABPR	P80369 haemophilus
701	11	11.1	16	1	HP28_SARPE	P23184 sarcophaga	774	11	11.1	21	1	PSAL_SYNBP	P31084 synecchococ
702	11	11.1	16	1	LE05_BIOGL	P80744 blomphalari	775	11	11.1	21	1	RP71_STRSQ	P37046 streptomyc
703	11	11.1	16	1	LPK1_LOCM1	P20404 locusta mig	776	11	11.1	21	1	SC1B_BPT5	P23208 bacteriopia
704	11	11.1	16	1	OD02_BOVIN	P11179 bos taurus	777	11	11.1	21	1	SRTD_ATTREN	P13211 attractaspis
705	11	11.1	16	1	PA2_NAASP	Q10756 najia sputat	778	11	11.1	21	1	TL13_SPIOL	P82661 spiniacia ol
706	11	11.1	16	1	RL6_VIBPR	Q56715 vibrio prot	779	11	11.1	21	1	XYNA_DIC94	P80718 dictyoglomu
707	11	11.1	16	1	VPR_HV1S3	P19555 human immun	780	11	11.1	22	1	APC1_MACPA	P18657 macaca fasc
708	11	11.1	16	1	YMOE_PSEPU	O02210 pseudomonas	781	11	11.1	22	1	AP65_CORTA	P50681 coturnix co
709	11	11.1	17	1	A43K_MYCBO	P80069 mycobacteri	782	11	11.1	22	1	CO4_CAVPO	P19069 cavia porce
710	11	11.1	17	1	ACTE_SOYBN	P15986 glycine max	783	11	11.1	22	1	CR31_LITSP	P56288 litorea spl
711	11	11.1	17	1	DNAK_MYCSM	P80692 mycobacteri	784	11	11.1	22	1	DNIV_BPDI0	Q38199 bacteriopia
712	11	11.1	17	1	RUBR_CHUTE	P58025 chlorobium	785	11	11.1	22	1	MDP_RANPE	P56924 rana tempor
713	11	11.1	17	1	SRY_URSAF	P36396 ursus arcto	786	11	11.1	22	1	MOTI_CHICK	Q9p196 gallus gall
714	11	11.1	17	1	TAC1_TACGI	P23684 tachypleus	787	11	11.1	22	1	VGIG_RABVA	P15199 rabies viru
715	11	11.1	17	1	TAC2_TACGI	P18252 tachypleus	788	11	11.1	22	1	YHVA_LACHE	P22296 lactobacill
716	11	11.1	18	1	AL12_CYNPO	P83153 cynthia pomon	789	11	11.1	23	1	CYSP_TRIFO	P33403 tritrichomo
717	11	11.1	18	1	CT1A_LITCI	P81838 litorea cit	790	11	11.1	23	1	GP50_BPSP1	Q48404 bacteriopia
718	11	11.1	18	1	CT1B_LITCI	P81839 litorea cit	791	11	11.1	23	1	MD12_LITGE	P82067 litorea gen
719	11	11.1	18	1	CT1C_LITCI	P81844 litorea cit	792	11	11.1	23	1	NO05_SOLTU	P80262 solanum tub
720	11	11.1	18	1	CT1D_LITCI	P81845 litorea cit	793	11	11.1	23	1	RL10_ENTCL	Q47608 enterobacte
721	11	11.1	18	1	FIBB_ANAPL	P12802 anas platyr	794	11	11.1	23	1	RL19_PETUY	P18550 pentula hyb
722	11	11.1	18	1	FIXA_RHILE	P14313 rhizobium l	795	11	11.1	24	1	BR1_RANBP	P32423 rana brevip
723	11	11.1	18	1	HEMH_THETS	P80155 thermomyzon	796	11	11.1	24	1	CH60_HEVYI	P26317 heliothis v
724	11	11.1	18	1	LYC_ESTAC	P82175 estigmene a	797	11	11.1	24	1	CLPE_HORVU	P48863 hordium vul
725	11	11.1	18	1	MCPE_METPE	P22949 methanosarc	798	11	11.1	24	1	CR16_LITXA	P56231 litorea xan
726	11	11.1	18	1	MD2_LITGE	P82066 litorea gen	799	11	11.1	24	1	CR18_LITXA	P81251 litorea chl
727	11	11.1	18	1	OBP_LYMDI	P34173 lymantria d	800	11	11.1	24	1	CR19_LITCH	P81252 litorea chl
728	11	11.1	18	1	PEP1_LIMPO	P14215 limulus pol	801	11	11.1	24	1	CSMB_PELDU	P15526 pelodictyon
729	11	11.1	18	1	TKN2_SCYCA	P08609 scyllorhinu	802	11	11.1	24	1	DHE3_PYRMO	Q09115 pyrococcus
730	11	11.1	19	1	AL12_HORSE	P81217 equus cabal	803	11	11.1	24	1	HEMU_LITNE	P23354 lingua ree
731	11	11.1	19	1	CH10_CLOPA	P81338 clostridium	804	11	11.1	24	1	LEC_CROUJ	P16332 crotalaria
732	11	11.1	19	1	COOR_SARBU	Q09148 sarcophaga	805	11	11.1	24	1	RS5_VIBPR	P52856 vibrio prot
733	11	11.1	19	1	DURA_STRGV	P35504 streptococ	806	11	11.1	25	1	ANDT_ANDAU	P56644 actinococcus
734	11	11.1	19	1	DURE_STRGV	P35502 streptococ	807	11	11.1	25	1	ANT3_MESAU	P81050 mesocricetu
735	11	11.1	19	1	DURC_STRGP	P35503 streptococ	808	11	11.1	25	1	APRY_SOLTU	P80497 solanum tub
736	11	11.1	19	1	FIBB_RANTA	P14462 raungiter la	809	11	11.1	25	1	AU52_LITRA	P82402 litorea ran
737	11	11.1	19	1	FIBB_PUG	P14477 sus scrofa	810	11	11.1	25	1	BGBP_PENVA	P81162 penaeus van
738	11	11.1	19	1	FIBB_VOLVU	P14482 vulpes vulp	811	11	11.1	25	1	CHLV_PENVA	P81241 carlica papa
739	11	11.1	19	1	H3_NARPS	P80553 narciassus p	812	11	11.1	25	1	CR11_LITSP	P56226 litorea spl
740	11	11.1	19	1	ITHA_PERAM	P19986 periplaneta	813	11	11.1	25	1	CR12_LITGE	P56227 litorea cae
741	11	11.1	19	1	LANC_STRSO	P36655 streptomyce	814	11	11.1	25	1	CR13_LITGE	P56228 litorea cae
742	11	11.1	19	1	LPRM_STRAU	P03063 strephylcoc	815	11	11.1	25	1	CR14_LITGI	P56229 litorea gll
743	11	11.1	19	1	PHSL_DESBN	P13066 desulfovibr	816	11	11.1	25	1	CR15_LITGE	P56230 litorea cae
744	11	11.1	19	1	PSMB_STYNU	P12312 synecchococ	817	11	11.1	25	1	CR1A_LITSP	P82104 litorea spl
745	11	11.1	19	1	PYRB_PSEFL	P56585 pseudomonas	818	11	11.1	25	1	CX44_CONPU	P55963 conus purpu
746	11	11.1	19	1	TRPB_KLEAE	P14552 klebsiella	819	11	11.1	25	1	FLAA_TREPH	P21963 treponema p
747	11	11.1	19	1	UKAI_HUMAN	P31940 homo sapien	820	11	11.1	25	1	IRBP_PIG	P12662 sus scrofa
748	11	11.1	20	1	APAI_ERPPA	P18647 erythrocebu	821	11	11.1	25	1	LYC_ASTRU	P37715 asterias ru
749	11	11.1	20	1	BIP_PHAUV	P80089 phaseolus v	822	11	11.1	25	1	MT_AGABI	P04338 agaricus bl
750	11	11.1	20	1	CATL_FASHE	Q00993 fasciola he	823	11	11.1	25	1	NEUO_RABIT	P34965 oryctolagus
751	11	11.1	20	1	COGA_FASHE	P34156 chionocete	824	11	11.1	25	1	SPIG_PSEUS	P82357 pseudocanth
752	11	11.1	20	1	COXA_THOIB	P80981 thunnus ode	825	11	11.1	25	1	YXCB_ODOST	P49834 odontella s
753	11	11.1	20	1	ELAS_GADMO	P32197 gadus morhu	826	11	10.1	4	1	BOSI_HUMAN	P02721 homo sapien
754	11	11.1	20	1	FIBB_FELIS	P14469 felis silve	827	11	10.1	6	1	ACPH_RABIT	P25134 oryctolagus
755	11	11.1	20	1	GTS2_ASCSU	P48429 ascaris suu	828	11	10.1	6	1	ASP2_LACSN	P82645 lactobacill
756	11	11.1	20	1	NLT1_HELIAN	P82007 helianthus	829	11	10.1	6	1	TRP1_PSEPU	P36414 pseudomonas
757	11	11.1	20	1	PEPT_FUSNP	P19502 fusobacteri	830	11	10.1	7	1	LANC_CARUI	P36960 carnobacter
758	11	11.1	20	1	PSMB_SYNUV	P19507 streptococ	831	11	10.1	7	1	MDP1_LEPPE	P22984 leptothars
759	11	11.1	20	1	STYA_STYCL	P81669 styela clay	832	11	10.1	7	1	MMAL_ACHRU	P35920 achelina fu
760	11	11.1	20	1	TL14_SPIOL	P82682 spinacia ol	833	11	10.1	7	1	WM42_ACHRU	P35920 achelina fu
761	11	11.1	20	1	TL18_SPIOL	P82336 spinacia ol	834	11	10.1	8	1	B44K_PORCI	P81886 porphyromon
762	11	11.1	20	1	UCRO_EDUAR	P81247 equisetum a	835	11	10.1	8	1	LCK1_LEUMA	P21140 leucophaea
763	11	11.1	20	1	UN05_PINPS	P81674 pinus pinas	836	11	10.1	8	1	LCK7_LEUMA	P19989 leucophaea

837	10	10.1	8	1	LPK_LEUMA	P13049	leucophaea	910	10	10.1	15	1	CX3B_CONOU	P58842	conus querc
838	10	10.1	8	1	RS1_ERWCH	P37985	erwinia chr	911	10	10.1	15	1	FRB7_PINS	P81104	pinus pinas
839	10	10.1	8	1	RS7_MYCIT	P33564	mycobacteri	912	10	10.1	15	1	FRB2_LITIN	P82022	litorea inf
840	10	10.1	9	1	FAR6_CALVO	P41861	calliphora	913	10	10.1	15	1	GR78_HORSE	P16392	equus cabal
841	10	10.1	9	1	FAR7_CALVO	P41862	calliphora	914	10	10.1	15	1	LCK_DROME	P61829	drosophila
842	10	10.1	9	1	FAR9_ASCSU	P43172	ascaris suu	915	10	10.1	15	1	LEC2_PSOSC	P22585	psophocarpa
843	10	10.1	9	1	HOTU_KIEAE	P12381	kiebsiella	916	10	10.1	15	1	LEC3_PSOSC	P22583	psophocarpu
844	10	10.1	9	1	MGMT_BOVIN	P29177	bos taurus	917	10	10.1	15	1	MALT_BACPO	P80072	bacillus th
845	10	10.1	9	1	PKK1_PERAM	P82691	periplaneta	918	10	10.1	15	1	PKKH_PHYPA	P80659	phycomitre
846	10	10.1	9	1	UN19_CLOPA	P81355	clostridium	919	10	10.1	15	1	PH3_PRUSE	P29265	prunus sero
847	10	10.1	9	1	XYLA_SPROSO	P19149	streptomyce	920	10	10.1	15	1	RRGG_CARCR	P21586	carella car
848	10	10.1	9	1	BPP2_BOTJA	P30422	bothrops ja	921	10	10.1	15	1	SODP_PINS	P81082	pinus pinas
849	10	10.1	10	1	BPP2_BOTJA	P30422	bothrops ja	922	10	10.1	15	1	TRPA_LEUMA	P1753	leucophaea
850	10	10.1	10	1	COXA_OMCMY	P80328	oncorhynch	923	10	10.1	15	1	UC14_MAIZE	P80620	zea mays (m
851	10	10.1	10	1	COXO_RABIT	P80336	oryctolagus	924	10	10.1	15	1	UC20_MAIZE	P80626	zea mays (m
852	10	10.1	10	1	ESTR_SCHGA	P81012	schizaphis	925	10	10.1	15	1	UC25_MAIZE	P80633	zea mays (m
853	10	10.1	10	1	FARC_CALVO	P41867	calliphora	926	10	10.1	15	1	UC27_MAIZE	P80633	zea mays (m
854	10	10.1	10	1	FIBB_CERSI	P14537	ceratotheri	927	10	10.1	15	1	UE15_HORVU	P34938	hordeum vul
855	10	10.1	10	1	GSO9_BACSU	P80343	bacillus su	928	10	10.1	15	1	CERB_RAT	P17338	morganelia
856	10	10.1	10	1	MOSO_CLYJA	P19862	clypeaster	929	10	10.1	16	1	CXA1_CONAL	P23436	rattus norv
857	10	10.1	10	1	PORB_METTM	P80301	methanobact	930	10	10.1	16	1	CXA2_CONAL	P56639	conus aulic
858	10	10.1	10	1	RL16_ACHLA	P29221	acholeplasm	931	10	10.1	16	1	CXA3_CONAL	P56636	conus magus
859	10	10.1	10	1	TKNK_PIG	P01392	sus scrofa	932	10	10.1	16	1	FIBA_CERSI	P14535	ceratotheri
860	10	10.1	10	1	TKS1_AEDAE	P42634	aedes aegy	933	10	10.1	16	1	FIBA_FELCA	P14530	felis silve
861	10	10.1	10	1	TKS2_AEDAE	P42635	aedes aegy	934	10	10.1	16	1	FIBA_FELCA	P14455	mandrillus
862	10	10.1	11	1	BPP3_BOTIN	P30423	bothrops in	935	10	10.1	16	1	H5_CORJA	P18638	colurnix co
863	10	10.1	11	1	BPP4_BOTIN	P30424	bothrops in	936	10	10.1	16	1	HPFG_ACICA	P81876	actinobact
864	10	10.1	11	1	BPP4_AKHA	P01021	agkistrodon	937	10	10.1	16	1	LEO6_BIOGL	P80745	biomphalai
865	10	10.1	11	1	PKK1_PERAM	P41837	periplaneta	938	10	10.1	16	1	PGTL_PELAC	P80563	pelobacter
866	10	10.1	11	1	RE41_LITRU	P82074	litorea rub	939	10	10.1	16	1	PH2_PRUSE	P23264	prunus sero
867	10	10.1	11	1	TIN1_HOPTI	P82651	hoplobatr	940	10	10.1	16	1	TRYP_FELCA	P81071	felis silve
868	10	10.1	11	1	TIN4_HOPTI	P82654	hoplobatr	941	10	10.1	16	1	FLAM_AZOC	P14460	sus scrofa
869	10	10.1	11	1	TKN3_PSEGU	P42988	pseudophryn	942	10	10.1	17	1	FIBA_PIG	P23002	azotobacter
870	10	10.1	11	1	CALM_TERTH	O05055	tetrahymena	943	10	10.1	17	1	JHBP_PLAVG	O01621	rattus norv
871	10	10.1	12	1	CD14_LITXA	P56246	litorea xan	944	10	10.1	17	1	LCK_RAT	O36834	trichophyto
872	10	10.1	12	1	CXST_CONTE	P58846	conus texti	945	10	10.1	17	1	NUAM_TIRIRU	P27642	bacillus li
873	10	10.1	12	1	HCVB_MEGCR	Q10504	megathura c	946	10	10.1	17	1	SP51_BACLI	P81666	pinus pinas
874	10	10.1	12	1	LICH_BACLI	P82907	bacillus li	947	10	10.1	17	1	TPIS_PINS	P82032	uperoleia i
875	10	10.1	12	1	PPK4_PERAM	P82650	periplaneta	948	10	10.1	17	1	UP31_UPEIN	P82033	uperoleia i
876	10	10.1	12	1	PPK4_PERFU	P81555	periplaneta	949	10	10.1	17	1	UP32_UPEIN	P82044	uperoleia i
877	10	10.1	12	1	PPK2_PERAM	P82652	hoplobatr	950	10	10.1	17	1	UP37_UPEMJ	P82035	uperoleia m
878	10	10.1	12	1	TIN2_HOPTI	P82653	hoplobatr	951	10	10.1	17	1	UP41_UPEIN	P17651	trypanosoma
879	10	10.1	12	1	TIN3_HOPTI	P82653	hoplobatr	952	10	10.1	17	1	YALA_TRYBB	P01209	pandatus bo
880	10	10.1	12	1	UDAL_MOUSE	P99032	mus musculi	953	10	10.1	17	1	DRPH_PANBO	P08871	uca pugilat
881	10	10.1	12	1	XYLA_STRVN	P14405	streptomyce	954	10	10.1	18	1	FIBA_CAMDR	P14444	camelus dro
882	10	10.1	12	1	VZPY_ECOLI	P17776	escherichia	955	10	10.1	18	1	FIBA_LAMGL	P35985	canine aden
883	10	10.1	13	1	CRBL_VESTR	P17221	vespa tropi	956	10	10.1	18	1	HEX_ADECU	P82419	pachycondyl
884	10	10.1	13	1	CRTC_BOVIN	P28449	bos taurus	957	10	10.1	18	1	PCG6_PACGO	P25771	pseudatelia
885	10	10.1	13	1	HPB9_RANES	P20304	sus scrofa	958	10	10.1	18	1	PHPT_PSESE	P83323	sitaelia gr
886	10	10.1	13	1	IDHC_PIG	P20011	trameles ve	959	10	10.1	18	1	R1P_SIRGR	P49624	serratia ma
887	10	10.1	13	1	LIGA_TRAVE	P41490	locusta mig	960	10	10.1	18	1	RL24_SERMA	P99504	canis famli
888	10	10.1	13	1	LMF4_LOCM1	P13772	gallus gall	961	10	10.1	18	1	ATPB_CANFA	P80327	oncorhynch
889	10	10.1	13	1	NEUT_CHICK	P31745	trichosurus	962	10	10.1	19	1	COXA_ONCMY	P80984	thunnus obe
890	10	10.1	13	1	NEUT_TRIUV	P80180	lymaea sta	963	10	10.1	19	1	DHAB_COMTE	P80704	comamonas t
891	10	10.1	13	1	NP3_LYMSR	P80578	hydra atten	964	10	10.1	19	1	ETFA_CLOPA	P81342	clostridium
892	10	10.1	13	1	PEDI_HYDAT	P47716	mycoplasma	965	10	10.1	19	1	FIBA_BISBO	P14457	bison bonas
893	10	10.1	13	1	RPOC_MYCGA	P56921	rana tempor	966	10	10.1	19	1	FIBA_MUNMU	P14539	tapirus ter
894	10	10.1	13	1	TEMF_RANTE	P81667	pinus pinas	967	10	10.1	19	1	FLA3_SPTAU	P21966	spirochaeta
895	10	10.1	13	1	ATP6_PSPOL	P80086	spinacia ol	968	10	10.1	19	1	NUO6_SOLTAU	P80729	solanum tub
896	10	10.1	14	1	CRBL_VESOR	P17236	vespa orien	969	10	10.1	19	1	PHLC_STAIN	P80934	staphylococ
897	10	10.1	14	1	MAST_VESOR	P17238	vespa orien	970	10	10.1	19	1	RLIO_CITFR	P43448	trichoderm
898	10	10.1	14	1	MCRX_METTM	P58815	methanobact	971	10	10.1	19	1	TCBI_TRILO	P80637	zea mays (m
899	10	10.1	14	1	PH1_PRUSE	P99506	canis famli	972	10	10.1	19	1	UC31_MAIZE	P82027	uperoleia i
900	10	10.1	14	1	UHA2_CANFA	P80083	spinacia ol	973	10	10.1	19	1	UP21_UPEIN	P82028	uperoleia i
901	10	10.1	14	1	ATP2_SPIOL	P31720	rattus norv	974	10	10.1	19	1	UP22_UPEIN	P82029	uperoleia i
902	10	10.1	15	1	C10A_RAT	P56248	litorea gill	975	10	10.1	19	1	UP23_UPEIN	P82030	uperoleia i
903	10	10.1	15	1	CDN3_LITGI	P82076	litorea cae	976	10	10.1	19	1	ACPH_BOVIN	P80227	bos taurus
904	10	10.1	15	1	CDN4_LITCE	P82077	litorea cae	977	10	10.1	20	1	CATA_ACIIRA	P81422	actinobact
905	10	10.1	15	1	CDN5_LITCE	P82078	litorea cae	978	10	10.1					
906	10	10.1	15	1	CDN6_LITCE	P82078	litorea cae	979	10	10.1					
907	10	10.1	15	1	CKX_WHEAT	P58763	tritlicum ae	980	10	10.1					
908	10	10.1	15	1	CKX_WHEAT	P58763	tritlicum ae	981	10	10.1					
909	10	10.1	15	1	CX3A_CONOU	P58841	conus querc	982	10	10.1	20	1			

983 10 10.1 20 1 CD4\_SHEEP  
 984 10 10.1 20 1 CBP\_THICU  
 985 10 10.1 20 1 COX2\_THICU  
 986 10 10.1 20 1 CP35\_PAPSP  
 987 10 10.1 20 1 CPBX\_CAVPO  
 988 10 10.1 20 1 CPXX\_RHORH  
 989 10 10.1 20 1 DER6\_DERPT  
 990 10 10.1 20 1 JHBP\_BOMMO  
 991 10 10.1 20 1 LPP2\_HUMAN  
 992 10 10.1 20 1 MDH\_KIBAR  
 993 10 10.1 20 1 M17\_BOVIN  
 994 10 10.1 20 1 OAR\_PROPY  
 995 10 10.1 20 1 PCW6\_PACGO  
 996 10 10.1 20 1 PKC\_CLOPA  
 997 10 10.1 20 1 PSAK\_PEA  
 998 10 10.1 20 1 PYRR\_PYRAP  
 999 10 10.1 20 1 R110\_PROVU  
 1000 10 10.1 20 1 STR\_RAT

## ALIGNMENTS

## RESULT 1

UC08\_MAIZE STANDARD; PRT; 15 AA.

AC P80614;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159)

DE (Fragment).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

OC Panicoidae; Andropogoneae; Zea.

OX NCBI\_Taxid=4577;

RN [1]

RP SEQUENCE.

RC TISSUE=Coleoptile;

RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,

RA Pernollet J.-C., Zivy M., de Vienne D.;

RT "The maize two dimensional gel protein database: towards an integrated

RT genome analysis program.";

RL Theor. Appl. Genet. 93:997-1005(1996).

CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 6.4, ITS MW IS: 38.8 kDa.

CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE

CC FAMILY.

DR Maize-2DPAGE; P80614; COLEOPTILE.

FT MAIZE: 123934; -

FT NON\_TER 1 1

FT NON\_TER 15 15

FT NON\_TER 15 15

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OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
 OC Ditylsia; Noctuidae; Noctuidae; Amphipylinae; Spodoptera.  
 OX NCBI\_Taxid=37547;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=99196260; PubMed=10098624;  
 RA Furuya K., Hackett M., Cirelli M.A., Schegg K.M., Wang H.,  
 RA Shabanowitz J., Hunt D.F., Schooley D.A.;

RT "A cardioactive peptide from the southern armyworm, Spodoptera

RT eridania.";

RT Peptides 20:53-61(1999).

RT -1- FUNCTION: HAS EXCITATORY EFFECTS ON A SEMI-ISOLATED HEART FROM

RT LARVAL MANDUCA SEXTA, CAUSING AN INOTROPIC EFFECT AT LOW

RT CONCENTRATIONS OF PEPTIDE AND CHRONOTROPIC AND INOTROPIC EFFECTS

RT AT HIGH DOSES.

CC -1- SIMILARITY: BELONGS TO THE GBP / PSPI / PARALYTIC PEPTIDE FAMILY.

CC HSSP: 061704; 1B1V.

CC InterPro: IPR003463; GBP\_PSP.

DR Pfam: PF02425; GBP\_PSP; 1.

DR DISULFID

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

FT SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

Query Match 30.3%; Score 30; DB 1; Length 23;

Best Local Similarity 50.0%; Pred. No. 70;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;



Db 9 PGYQRTADGR 18

RESULT 4

PAP2\_SPOEX STANDARD; PRT; 23 AA.

AC P30257;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Paralytic peptide II (PP II).  
 OS Spodoptera exigua (Beet armyworm).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
 OC Ditrysia; Noctuoidea; Noctuidae; Amphipyriinae; Spodoptera.  
 OX NCBI\_TaxID=7107;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=91302298; PubMed=2071576;  
 RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,  
 RA Quistad G.B.;  
 RT "Isolation and identification of paralytic peptides from hemolymph of  
 the lepidopteran insects Manduca sexta, Spodoptera exigua, and  
 Heliothis virescens.";  
 RT J. Biol. Chem. 266:12873-12877(1991).  
 RL -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO  
 LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE  
 HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.  
 CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.  
 CC PIR: D39855; D39855.  
 DR HSSP; O61704; 1B1V.  
 DR InterPro: IPR003463; GBP\_PSP.  
 DR Pfam: PF02425; GBP\_PSP; 1.  
 KW Hemolymph.  
 FT DISULFID  
 SQ SEQUENCE 23 AA: 2477 MW: 0A96CB4600855AE0 CRC64;

Query Match 30.3%; Score 30; DB 1; Length 23;  
 Best Local Similarity 50.0%; Pred. No. 70;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGHERMGGR 12  
 ||:|  
 Db 9 PGYQRTADGR 18

RESULT 5

PAP3\_SPOEX STANDARD; PRT; 23 AA.

AC P30257;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Paralytic peptide III (PP III).  
 OS Spodoptera exigua (Beet armyworm).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
 OC Ditrysia; Noctuoidea; Noctuidae; Amphipyriinae; Spodoptera.  
 OX NCBI\_TaxID=7107;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=91302298; PubMed=2071576;  
 RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,  
 RA Quistad G.B.;  
 RT "Isolation and identification of paralytic peptides from hemolymph of  
 the lepidopteran insects Manduca sexta, Spodoptera exigua, and  
 Heliothis virescens.";  
 RT J. Biol. Chem. 266:12873-12877(1991).  
 RL -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO  
 LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE  
 HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.  
 CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.  
 CC PIR: D39855; D39855.  
 DR HSSP; O61704; 1B1V.  
 DR InterPro: IPR003463; GBP\_PSP.  
 DR Pfam: PF02425; GBP\_PSP; 1.  
 KW Hemolymph.  
 FT DISULFID  
 SQ SEQUENCE 23 AA: 2524 MW: 2236CB4360655AFA CRC64;

Query Match 29.3%; Score 29; DB 1; Length 23;  
 Best Local Similarity 45.5%; Pred. No. 1e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VPGHERMGGR 12  
 ||:|  
 Db 8 IPGYRTADGR 18

CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.  
 DR PIR: E39855; E39855.  
 DR HSSP; O61704; 1B1V.  
 DR InterPro: IPR003463; GBP\_PSP.  
 DR Pfam: PF02425; GBP\_PSP; 1.  
 KW Hemolymph.  
 FT DISULFID  
 SQ SEQUENCE 23 AA: 2505 MW: 0A96CB5EB7D55AE0 CRC64;

Query Match 30.3%; Score 30; DB 1; Length 23;  
 Best Local Similarity 50.0%; Pred. No. 70;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGHERMGGR 12  
 ||:|  
 Db 9 PGYQRTADGR 18

RESULT 6

PAP1\_HELVI STANDARD; PRT; 23 AA.

AC P30251;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Paralytic peptide I (PP I).  
 OS Heliothis virescens (Noctuid moth) (Owllet moth).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
 OC Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.  
 OX NCBI\_TaxID=7102;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=91302298; PubMed=2071576;  
 RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,  
 RA Quistad G.B.;  
 RT "Isolation and identification of paralytic peptides from hemolymph of  
 the lepidopteran insects Manduca sexta, Spodoptera exigua, and  
 Heliothis virescens.";  
 RT J. Biol. Chem. 266:12873-12877(1991).  
 RL -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO  
 LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE  
 HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.  
 CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.  
 CC PIR: E39855; F39855.  
 DR HSSP; O61704; 1B1V.  
 DR InterPro: IPR003463; GBP\_PSP.  
 DR Pfam: PF02425; GBP\_PSP; 1.  
 KW Hemolymph.  
 FT DISULFID  
 SQ SEQUENCE 23 AA: 2524 MW: 2236CB4360655AFA CRC64;

Query Match 29.3%; Score 29; DB 1; Length 23;  
 Best Local Similarity 45.5%; Pred. No. 1e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VPGHERMGGR 12  
 ||:|  
 Db 8 IPGYRTADGR 18

RESULT 7

PAP2\_HELVI STANDARD; PRT; 23 AA.

AC P30252;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Paralytic peptide II (PP II).  
 OS Heliothis virescens (Noctuid moth) (Owllet moth).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;

OC Ditylsia; Noctuidae; Noctuidae; Heliothinae; Heliothis.  
OX NCBI\_TaxID=7102;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Hemolymph;  
MEDLINE=91302238; PubMed=2071576;  
RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,  
Kistad G.B.;  
RT "Isolation and identification of paralytic peptides from hemolymph of  
the lepidopteran insects Manduca sexta, Spodoptera exigua, and  
Heliothis virescens."  
RL J. Biol. Chem. 266:12873-12877(1991).  
CC -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO  
LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE  
CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.  
DR PIR: G39855; G39855.  
DR HSP: 061704; 1B1V.  
DR InterPro: IPR003463; GBP\_PSP.  
DR Pfam: PF02425; GBP\_PSP; 1.  
DR Hemolymph.  
SEQUENCE 23 AA; 2508 MW; 2236CB5D6C85AFA CRC64;

Query Match 29.3%; Score 29; DB 1; Length 23;  
Best Local Similarity 45.5%; Pred. No. 1e+02; 4; Indels 0; Gaps 0;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 2 VPGHERMGRGR 12  
: : : : :  
DB 8 IPGYMFTADGR 18

RESULT 8  
ADF\_TEMNO STANDARD; PRT; 14 AA.  
AC P82965;  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Antidiuretic factor (ADF) (Antidiuretic hormone A) (ADHA).  
OS Tenebrio molitor (Yellow mealworm).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
OC Cucujiformia; Tenebrionidae; Tenebrio.  
OX NCBI\_TaxID=7067;  
RN [1]  
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.  
RC TISSUE=Head;  
MEDLINE=21642653; PubMed=11756661;  
Eisenberg R.A., Nicolson S.W., Schegg K.M., Hull J.J., Schooley D.A.;  
RT "Identification of a potent antidiuretic factor acting on beetle  
Malpighian tubules."  
Proc. Natl. Acad. Sci. U.S.A. 99:84-89(2002).  
CC -1- FUNCTION: Strong inhibitor of fluid secretion by the Malpighian  
tubules. Uses cGMP as a second messenger and inhibits fluid  
production by decreasing cAMP concentration.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- MASS SPECTROMETRY: MW=1341.58; METHOD=MALDI.  
CC -1- SIMILARITY: STRONG, TO THE C-TERMINAL OF T. MOLITOR CUTICULAR  
PROTEIN LPP29.  
KW Neuropeptide; Hormone.  
SQ SEQUENCE 14 AA; 1543 MW; F49C91A3F16E43D1 CRC64;

Query Match 27.3%; Score 27; DB 1; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NVPGRH 5  
: : : : :  
DB 3 NTPGRH 7

RESULT 9  
DNAJ\_STRAG

ID DNAJ\_STRAG STANDARD; PRT; 24 AA.  
AC P95694;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Chaperone protein dnaJ (Fragment).  
GN DNAJ.  
OS Streptococcus agalactiae.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1311;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Riaux C.R., Martin D., Brodeur B.R.;  
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: ACTS AS A CO-CHAPERONE. STIMULATES, JOINTLY WITH GREP,  
THE ATPASE ACTIVITY OF DNAJ (BY SIMILARITY).  
CC -1- COFACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE DNAJ FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 J DOMAIN.  
-----

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DR EMBL: U72719; AAB39220.1; -;  
DR InterPro: IPR001305; DnaJ\_CXXCGXG.  
DR InterPro: IPR001623; DnaJ\_N.  
DR Pfam: PF00226; DnaJ; 1.  
DR PROSITE: PS00636; DnaJ\_1; PARTIAL.  
DR PROSITE: PSS0076; DnaJ\_2; PARTIAL.  
DR PROSITE: PSS00637; DnaJ\_CXXCGXG; PARTIAL.  
KW Chaperone; DNA replication; Heat shock; Repeat; zinc; Metal-binding.  
FT DOMAIN 3 >24  
FT NON\_TER 24 24  
SQ SEQUENCE 24 AA; 2760 MW; 342AE56E00913FC CRC64;

Query Match 25.3%; Score 25; DB 1; Length 24;  
Best Local Similarity 23.5%; Pred. No. 5e+02;  
Matches 4; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 NVPGRMGRGRTSK 17  
: : : : :  
DB 3 NTFYDRIVSKDASD 19

RESULT 10  
DCM\_PSECH STANDARD; PRT; 15 AA.  
ID DCM\_PSECH  
AC P19917;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Carbon monoxide dehydrogenase medium chain (EC 1.2.99.2) (CO  
dehydrogenase subunit M) (CO-DH M) (Fragment).  
GN CUTM.  
OS Pseudomonas carboxydohydrogena.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Bradyrhizobium group.  
OX NCBI\_TaxID=290;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90055678; PubMed=2818128;  
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
RT "Homology and distribution of CO dehydrogenase structural genes in  
carboxydophilic bacteria."  
Arch. Microbiol. 152:335-341(1989).  
RL Arch.  
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon





FT UNSURE 18 18 OR I.  
 FT UNSURE 22 22 OR I.  
 FT NON\_TER 25 25  
 SQ SEQUENCE 25 AA; 2710 MW; 9888B56C2352D81 CRC64;

Query Match 22.2%; Score 22; DB 1; Length 25;  
 Best Local Similarity 35.3%; Pred. No. 1.7e+03;  
 Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 NYPHERMGRRTSSKE 17  
 : | | | : | | |  
 Db 4 DVLGPRIGXQLTTLNE 20

RESULT 17  
 ID IBP4\_PIG STANDARD; PRT; 16 AA.  
 AC P24854;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 RT Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)  
 DE (IGF-binding protein 4) (fragment).  
 GN IGFBP4.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92109718; PubMed=1722398;  
 RA Coleman M.E., Pan Y.-C.E., Eberton T.D.;  
 RT "Identification and NH2-terminal amino acid sequence of three  
 RT insulin-like growth factor-binding proteins in porcine serum.";  
 RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).  
 CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFS  
 CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH  
 CC PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE  
 CC INTERACTION OF IGFS WITH THEIR CELL SURFACE RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: Secreted  
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING  
 CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.  
 CC PROTEIN FAMILY.  
 CC PIR: JH0517; JH0517.  
 DR InterPro: IPR000867; Insl\_gro\_fac.pr.  
 DR InterPro: IPR000716; Thyroglobulin.1.  
 DR PROSITE: PS00222; IGF-BINDING. PARTIAL.  
 DR PROSITE: PS00484; THYROGLOBULIN\_1; PARTIAL.  
 KM Growth factor binding.  
 NT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 21.2%; Score 21; DB 1; Length 16;  
 Best Local Similarity 37.5%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGHERMGR 10  
 | | | : | | |  
 Db 9 PSEKRLAR 16

RESULT 18  
 ID MLB\_SCYCA STANDARD; PRT; 18 AA.  
 AC P01206;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Melanotropin beta (Beta-MSH).  
 OS Scylliorhinus canicula (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scylliorhinidae; Scylliorhinus.

OX NCBI\_TaxID=7830;

RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75113445; PubMed=4452470;  
 RA Love R.M., Pickering B.T.;  
 RT "A beta-MSH in the pituitary gland of the spotted dogfish  
 RT (Scylliorhinus canicula): isolation and structure.";  
 RL Gen. Comp. Endocrinol. 24:398-404(1974).  
 CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.  
 DR PIR: A01470; MTDIBC.  
 KW Hormone.  
 SQ SEQUENCE 18 AA; 2195 MW; 353C93A30C314DF4 CRC64;

Query Match 21.2%; Score 21; DB 1; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GHERMG 9  
 | | | : | | |  
 Db 8 GHRMG 13

RESULT 19  
 ID PORC\_METTMM STANDARD; PRT; 20 AA.  
 AC P80902;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Pyruvate synthase subunit PORC (EC 1.2.7.1) (Pyruvate oxidoreductase  
 DE gamma chain) (POR) (Pyruvic-ferredoxin oxidoreductase gamma subunit)  
 DE (Fragment).  
 GN PORC.  
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).  
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
 OC Methanobacteriaceae; Methanothermobacter.  
 OX NCBI\_TaxID=79929;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=97261844; PubMed=9108258;  
 RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;  
 RT "Structures and functions of four anaerobic 2-oxoacid oxidoreductases  
 RT in Methanobacterium thermoautotrophicum.";  
 RL Eur. J. Biochem. 244:862-868(1997).  
 CC -1- FUNCTION: THE PH OPTIMUM IS PH 10.0 AND THE OPTIMAL TEMPERATURE  
 CC IS 80 DEGREES CELSIUS.  
 CC -1- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-  
 CC CoA + CO(2) + reduced ferredoxin.  
 CC -1- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).  
 CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE  
 CC GAMMA CHAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.  
 KM Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.  
 NT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2167 MW; 481532134D42F353 CRC64;

Query Match 21.2%; Score 21; DB 1; Length 20;  
 Best Local Similarity 28.6%; Pred. No. 1.9e+03;  
 Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 HERMGRRTSSKEL 18  
 | | | : | | |  
 Db 7 HGRGQXAVTAIEI 20

RESULT 20  
 ID NEUT\_RANTE STANDARD; PRT; 25 AA.  
 AC P20056;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neuromedin U-25 (Nmu-25).

OS Rana temporaria (European common frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
OX NCBI\_TaxID=8407;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=90078173; PubMed=2592357;  
RA Domin J., Yiangou Y.G., Spokes R.A., Altken A., Parmar K.B.,  
RT Chrysanthou B.J., Bloom S.R.,  
RT "The distribution, purification, and pharmacological action of an  
RT amphibian neuromedin U."  
RL J. Biol. Chem. 264:20881-20885(1989).  
CC -1- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES  
CC SELECTIVE VASOCONSTRICTION.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE NMU FAMILY.  
DR PIR: A34179; A34179.  
InterPro: IPR001942; NMU.  
Pfam: PF02070; NMU; 1.  
SMART: SMO0084; NMU; 1.  
PROSITE: PS00967; NMU; 1.  
KW Amidation; Hormone.  
FT MOD\_RES 25  
SQ SEQUENCE 25 AA; 2832 MW; 6A01D89FDA06FD4 CRC64;  
AMIDATION.  
Query Match 21.2%; Score 21; DB 1; Length 25;  
Best Local Similarity 35.7%; Pred. No. 2.4e+03;  
Matches 5; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
QY 3 PGHERMGRGRTSSK 16  
DB 3 PDEELQPGGVLSR 16

RESULT 21  
PGQ\_XENLA  
ID PGQ\_XENLA STANDARD; PRT; 24 AA.  
AC P39080;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DE Antimicrobial peptide PGQ.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8353;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Stomach;  
RX MEDLINE=92011794; PubMed=1717472;  
RA Moore K.S., Bevins C.L., Brasseur M.M., Tomassini N., Turner K.,  
RT Eck H., Zasloff M.,  
RT "Antimicrobial peptides in the stomach of Xenopus laevis."  
RL J. Biol. Chem. 266:19851-19857(1991).  
CC -1- FUNCTION: ANTIMICROBIAL PEPTIDE.  
CC -1- TISSUE SPECIFICITY: IS SYNTHESIZED IN THE STOMACH AND STORED  
CC IN A NOVEL GRANULAR MULTINUCLEATED CELL IN THE GASTRIC MUCOSA.  
CC IT IS STORED AS ACTIVE, PROCESSED PEPTIDES IN LARGE GRANULES  
CC WITHIN THE GRANULAR GLAND SECRETIONS OF THE SKIN.  
CC -1- SIMILARITY: BELONGS TO THE MAGAININ FAMILY OF ANTIMICROBIAL  
CC PEPTIDES.  
DR PIR: A41037; A41037.  
KW Antibiotic; Amphibian skin.  
SQ SEQUENCE 24 AA; 2457 MW; 7E6A87CB7CF22B9C CRC64;  
Query Match 20.7%; Score 20.5; DB 1; Length 24;  
Best Local Similarity 41.7%; Pred. No. 2.8e+03;  
Matches 5; Conservative 4; Mismatches 2; Indels 1; Gaps 1;  
QY 1 NVPGH-ERMGRG 11  
DB 11:::11

DB 5 NVIGYKLKLTGTG 16

RESULT 22  
CHOX\_ALCSP  
ID CHOX\_ALCSP STANDARD; PRT; 7 AA.  
AC P16101;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DE Choline oxidase (EC 1.1.3.17) (Fragment).  
OS Alcaligenes sp.  
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;  
OC Alcaligenes.  
OX NCBI\_TaxID=512;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81006769; PubMed=6997283;  
RA Ohta-Fukuyama M., Miyake Y., Eml S., Yamano T.,  
RT "Identification and properties of the prosthetic group of choline  
RT oxidase from Alcaligenes sp."  
RL J. Biochem. 88:197-203(1980).  
CC -1- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).  
DR PIR: A15398; A15398.  
KW Oxidoreductase.  
FT NON\_TER 7  
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;  
Query Match 20.2%; Score 20; DB 1; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.1e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 PGHER 7  
DB 3 PNHSR 7

RESULT 23  
PNOC\_PIG  
ID PNOC\_PIG STANDARD; PRT; 17 AA.  
AC P55791;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE Nociceptin (Orphanin FQ).  
DE Nociceptin (Orphanin FQ).  
GN PNOC.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Hypothalamus;  
RX MEDLINE=96055113; PubMed=7481766;  
RA Reinscheid R.K., Notthacker H.-P., Bourson A., Ardali A.,  
RA Henningsen R.A., Bunzow J.R., Grandy D.K., Langen H., Monsma F.J. Jr.,  
RA Civelli O.,  
RT "Orphanin FQ: a neuropeptide that activates an opioidlike G protein-  
RT coupled receptor."  
RL Science 270:792-794(1995).  
CC -1- FUNCTION: NOCICEPTIN IS THE LIGAND OF THE OPIOID RECEPTOR-LIKE  
CC RECEPTOR (OPRL1). IT MAY ACT AS A TRANSMITTER IN THE BRAIN BY  
CC MODULATING NOCICEPTIVE AND LOCOMOTOR BEHAVIOR. MAY BE INVOLVED IN  
CC NEURONAL DIFFERENTIATION AND DEVELOPMENT. WHEN ADMINISTERED  
CC INTRACEREBROVENTRICULARLY INTO MICE, THIS PEPTIDE INDUCES  
CC HYPERALGESIA AND DECREASES LOCOMOTOR ACTIVITY.  
CC -1- SUBCELLULAR LOCATION: SECRETED INTO THE ENDOPLASMIC RETICULUM.  
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY IN THE BRAIN AND SPINAL CORD.  
CC -1- SIMILARITY: BELONGS TO THE OPIOIDS NEUROPETIDES PRECURSORS  
CC FAMILY.  
DR InterPro: IPR000094; Opioid\_neuropep.  
DR PROSITE: PS01252; OPIOIDS\_PRECURSOR; PARTIAL.  
KW Opioid peptide; Neurotransmitter; Neuropeptide.







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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:04:22 ; Search time 29 Seconds  
(without alignments)  
134.996 Million cell updates/sec

Title: US-09-674-913a-1  
Perfect score: 99  
Sequence: 1 NVPGHERMGRTSSKELA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 9297

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

SPTRMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriaph:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31.3	24	4	08RXU1	08rxu1 homo sapien
2	29.3	18	4	015912	015912 homo sapien
3	28.3	23	10	09M7J2	09m7j2 hordeum chi
4	28.3	23	11	09Z2R1	09z2r1 rattus norv
5	27.3	17	4	013376	013376 homo sapien
6	27.3	20	13	09DEH9	09deh9 xenopus lae
7	27.3	24	8	09GFA0	09gfa0 calycanthus
8	26.3	19	15	0905H2	0905h2 human immun
9	26.3	20	15	09DYR0	09dyr0 human immun
10	26.3	24	4	09R573	09r573 nitrosoma
11	26.3	24	4	09GCT8	09gct8 homo sapien
12	26.3	24	11	08VHY7	08vhy7 mus musculu
13	25.3	19	4	09R763	09r763 rhizobium l
14	25.3	19	4	016271	016271 homo sapien
15	25.3	19	12	085658	085658 reovirus (t
16	25.3	21	11	09QUZ0	09quz0 rattus sp.

17	25.3	21	13	09DD39	09dd39 nipponia ni
18	25.3	22	13	057692	057692 otis tarda.
19	25.3	25	10	099215	099215 triticum mo
20	24.2	16	4	09UD45	09ud45 homo sapien
21	24.2	16	11	09R009	09r009 rattus norv
22	24.2	17	5	09V973	09v973 drosophila
23	24.2	17	10	09AUB3	09aub3 arabidopsis
24	24.2	19	6	09TRK3	09trk3 bos taurus
25	24.2	19	15	09ORG1	09org1 human immun
26	24.2	20	10	08RW5	08rw5 arabidopsis
27	24.2	22	13	0919P3	0919p3 ara millitar
28	24.2	23	3	09A1L1	09a1l1 magnetospir
29	24.2	23	3	09UR71	09ur71 lentinula e
30	24.2	24	10	08RVD4	08rvd4 pinus sylve
31	24.2	25	8	09GFP2	09gfp2 dioscorea b
32	23.5	18	2	030888	030888 bradyrhizob
33	23.2	15	6	09R545	09r545 mycobacteri
34	23.2	15	6	09T0Q5	09t0q5 bos taurus
35	23.2	16	11	09QVA6	09qva6 mus sp. pro
36	23.2	18	2	09R501	09r501 bacillus su
37	23.2	20	1	09UWH0	09uwh0 thermococu
38	23.2	20	11	09QU71	09qu71 rattus sp.
39	23.2	20	12	09ICE8	09ice8 tt virus. o
40	23.2	22	11	0922R6	0922r6 mus musculu
41	23.2	22	13	0918S8	0918s8 gallus gall
42	23.2	23	4	09UMI6	09umi6 homo sapien
43	23.2	23	4	09RYM6	09rym6 homo sapien
44	23.2	23	4	09EB48	09eb48 homo sapien
45	23.2	24	11	063983	063983 mus musculu
46	23.2	25	11	09QV57	09qv57 rattus norv
47	23.2	25	12	09J1H6	09j1h6 tt virus. o
48	23.2	25	12	09J1H4	09j1h4 tt virus. o
49	23.2	25	12	09J1G9	09j1g9 tt virus. o
50	23.2	25	12	09J1G7	09j1g7 tt virus. o
51	23.2	25	12	09J1E2	09j1e2 tt virus. o
52	23.2	25	12	09J1D8	09j1d8 tt virus. o
53	23.2	25	15	09WRP2	09wrp2 human immun
54	23.2	25	15	09WBV6	09wbv6 human immun
55	22.2	10	11	09QVE7	09qve7 mus sp. pro
56	22.2	12	15	078845	078845 human immun
57	22.2	14	11	09Z0G5	09z0g5 mus musculu
58	22.2	14	15	010229	010229 human immun
59	22.2	14	15	010230	010230 human immun
60	22.2	14	15	010235	010235 human immun
61	22.2	16	4	09BOP2	09bop2 homo sapien
62	22.2	19	12	09PKX2	09pkx2 tobacco vel
63	22.2	20	12	085617	085617 reovirus (t
64	22.2	21	10	041580	041580 triticum ae
65	22.2	21	13	P79889	P79889 gallus gall
66	22.2	21	15	087579	087579 chimpanzee
67	22.2	21	15	087581	087581 chimpanzee
68	22.2	22	6	09SKU7	09sku7 bos taurus
69	22.2	22	12	085664	085664 reovirus (t
70	22.2	23	1	09UWL2	09uwl2 pyrococcus
71	22.2	23	5	09Y002	09y002 melarhaph
72	22.2	23	12	066204	066204 transmissib
73	22.2	23	12	066184	066184 porcine res
74	22.2	24	8	09JUN1	09jun1 neisseria m
75	22.2	24	16	09T1S8	09t1s8 angophora c
76	22.2	24	10	09S8R5	09s8r5 colocasia e
77	22.2	25	2	09R4C8	09r4c8 mycoplasma
78	22.2	25	4	014497	014497 homo sapien
79	22.2	25	4	096OP2	096op2 homo sapien
80	22.2	25	5	023966	023966 dendrocoelu
81	22.2	25	15	09UD03	09ud03 human immun
82	22.2	25	15	071940	071940 human immun
83	22.2	25	15	071946	071946 human immun
84	22.2	25	15	0910P9	0910p9 human immun
85	22.2	25	15	0910O0	0910o0 human immun
86	22.2	25	15	0910O1	0910o1 human immun
87	22.2	25	15	0910O2	0910o2 human immun
88	22.2	25	15	0910O3	0910o3 human immun
89	22.2	25	15	0910O4	0910o4 human immun

90	22	22.2	25	15	Q91Q08	Q91qg8 human immun	163	20	20.2	18	11	Q62256	Q62256 mus musculus
91	22	22.2	25	15	Q91Q00	Q91qr0 human immun	164	20	20.2	18	13	Q9PRU5	Q9PRU5 torpedo mar
92	22	22.2	25	15	Q91Q01	Q91qr1 human immun	165	20	20.2	19	4	Q9UCU1	Q9UCU1 homo sapien
93	22	22.2	25	15	Q91Q02	Q91qr2 human immun	166	20	20.2	19	10	Q9S8W0	Q9S8W0 triticum ae
94	22	22.2	25	15	Q91Q03	Q91qr3 human immun	167	20	20.2	20	2	Q51558	Q51558 pseudomonas
95	22	22.2	25	15	Q91Q04	Q91qr4 human immun	168	20	20.2	20	2	Q47598	Q47598 escherichia
96	22	22.2	25	15	Q91Q05	Q91qr5 human immun	169	20	20.2	20	2	Q9S6C4	Q9S6C4 salmonella
97	22	22.2	25	15	Q8QDY1	Q8qdy1 human immun	170	20	20.2	20	2	Q9R4H6	Q9R4H6 bacillus su
98	22	22.2	25	15	Q8QDX7	Q8qdx7 human immun	171	20	20.2	20	5	Q9U8M6	Q9U8M6 liodrosophi
99	21.5	21.7	20	12	Q9R551	Q9r551 bacillus me	172	20	20.2	20	11	Q9QV61	Q9QV61 rattus sp.
100	21	21.2	11	15	Q89616	Q89616 avian infec	173	20	20.2	21	4	Q14595	Q14595 homo sapien
101	21	21.2	12	2	Q9D232	Q9d232 human immun	174	20	20.2	21	5	Q25085	Q25085 herdanista m
102	21	21.2	13	5	Q9W506	Q9w506 drosophila	175	20	20.2	21	10	Q9S7O4	Q9S7O4 arabidopsis
103	21	21.2	14	6	Q9N1V6	Q9n1v6 equus caball	176	20	20.2	22	15	Q9W7Z6	Q9W7Z6 human immun
104	21	21.2	15	1	Q9U8G1	Q9u8g1 pyrococcus,	177	20	20.2	22	5	Q9BH35	Q9BH35 caenorhabdi
105	21	21.2	15	10	Q9S8V6	Q9s8v6 triticum ae	178	20	20.2	22	13	Q13047	Q13047 xenopus lae
106	21	21.2	16	4	Q9NY32	Q9ny32 homo sapien	179	20	20.2	23	4	Q16090	Q16090 homo sapien
107	21	21.2	16	4	Q96T79	Q96t79 homo sapien	180	20	20.2	23	5	Q61341	Q61341 panullius i
108	21	21.2	16	4	Q9UD46	Q9ud46 homo sapien	181	20	20.2	23	5	Q9TWE7	Q9TWE7 pseudaletia
109	21	21.2	16	6	Q9TRD1	Q9trd1 sus scrofa	182	20	20.2	23	6	Q9TRP7	Q9TRP7 bos taurus
110	21	21.2	16	10	Q82402	Q82402 fragaria nu	183	20	20.2	23	10	Q94IS9	Q94IS9 pinus taeda
111	21	21.2	16	10	Q82403	Q82403 fragaria ve	184	20	20.2	23	13	Q9PRV6	Q9PRV6 anguilla ja
112	21	21.2	16	10	Q82404	Q82404 fragaria ni	185	20	20.2	23	13	Q9PSA8	Q9PSA8 xenopus bor
113	21	21.2	16	10	Q82405	Q82405 fragaria il	186	20	20.2	23	13	Q9BSK7	Q9BSK7 human immun
114	21	21.2	16	10	Q82406	Q82406 fragaria mo	187	20	20.2	24	2	Q9R7V0	Q9R7V0 streptococ
115	21	21.2	16	10	Q82407	Q82407 fragaria vi	188	20	20.2	24	2	P81594	P81594 desulfitoba
116	21	21.2	16	10	Q82408	Q82408 fragaria ve	189	20	20.2	24	5	P83215	P83215 octopus vul
117	21	21.2	17	8	Q36741	Q36741 homo sapien	190	20	20.2	24	5	P83215	Q65700 bromo mosai
118	21	21.2	17	8	Q36741	Q36741 homo sapien	191	20	20.2	24	12	Q65700	Q65700 bromo mosai
119	21	21.2	17	10	Q9S889	Q9s889 narcissus p	192	20	20.2	25	5	Q9BM65	Q9BM65 monostyla s
120	21	21.2	18	2	Q9R583	Q9r583 aspergillus m	193	20	20.2	25	6	Q9TR43	Q9TR43 bos taurus
121	21	21.2	18	3	Q02414	Q02414 aspergillus m	194	20	20.2	25	6	Q9TR43	Q9TR43 bos taurus
122	21	21.2	19	2	P74875	P74875 salmonella	195	20	20.2	25	6	Q9TR00	Q9TR00 sus scrofa
123	21	21.2	19	4	Q9S578	Q9s578 homo sapien	196	20	20.2	25	10	Q94IS2	Q94IS2 pinus radia
124	21	21.2	19	4	Q9UCG2	Q9ucg2 homo sapien	197	20	20.2	25	11	Q9QUZ6	Q9QUZ6 mus sp. 205
125	21	21.2	19	10	Q06914	Q06914 brassica na	198	20	20.2	25	12	Q9JIG2	Q9JIG2 tt virus. o
126	21	21.2	19	13	Q8UVE0	Q8uve0 gallus gall	199	20	20.2	25	12	Q9JIE5	Q9JIE5 tt virus. o
127	21	21.2	20	4	Q9UD25	Q9ud25 homo sapien	200	20	20.2	25	13	P83129	P83129 paratichthy
128	21	21.2	20	4	Q9UD25	Q9ud25 homo sapien	201	20	20.2	25	15	Q9QEX7	Q9QEX7 human immun
129	21	21.2	20	13	Q9WPQ4	Q9wpq4 mus musculu	202	20	20.2	25	15	Q9WR00	Q9WR00 human immun
130	21	21.2	20	13	Q9WPQ4	Q9wpq4 mus musculu	203	20	20.2	25	13	Q9PRV0	Q9PRV0 anguilla ja
131	21	21.2	22	4	Q9S597	Q9s597 homo sapien	204	20	20.2	25	10	Q86580	Q86580 simian para
132	21	21.2	22	4	Q9S597	Q9s597 homo sapien	205	20	20.2	25	11	Q9R0K9	Q9R0K9 mus musculu
133	21	21.2	22	6	Q9N1F3	Q9n1f3 gorilla gor	206	20	20.2	25	11	Q9TRW5	Q9TRW5 bos taurus
134	21	21.2	22	13	Q9PRN2	Q9prn2 petromyzon	207	20	20.2	25	11	Q9R0K9	Q9R0K9 mus musculu
135	21	21.2	23	2	Q54449	Q54449 rhodobacter	208	20	20.2	25	12	Q9TWY0	Q9TWY0 fasciola he
136	21	21.2	23	8	Q55223	Q55223 streptococ	209	20	20.2	25	12	Q8R2F6	Q8R2F6 rattus norv
137	21	21.2	24	4	Q16061	Q16061 oenothera b	210	20	20.2	25	12	Q9PS67	Q9PS67 gallus gall
138	21	21.2	24	4	Q16061	Q16061 homo sapien	211	20	20.2	25	13	Q9UCG9	Q9UCG9 homo sapien
139	21	21.2	24	11	Q88570	Q88570 mus musculu	212	20	20.2	25	4	Q9U5J3	Q9U5J3 trypanosoma
140	21	21.2	24	11	Q88571	Q88571 mus musculu	213	20	20.2	25	4	Q9P2X4	Q9P2X4 homo sapien
141	21	21.2	25	2	Q47669	Q47669 escherichia	214	20	20.2	25	4	Q16484	Q16484 homo sapien
142	21	21.2	25	2	Q9R4N7	Q9r4n7 pseudomonas	215	20	20.2	25	4	Q9R546	Q9R546 mycobacteri
143	21	21.2	25	4	Q96HF0	Q96hf0 homo sapien	216	20	20.2	25	10	Q9AUA2	Q9AUA2 maththiola t
144	21	21.2	25	5	Q23750	Q23750 ctenodrilus	217	20	20.2	25	11	Q923G8	Q923G8 rattus norv
145	21	21.2	25	12	Q86949	Q86949 human herpe	218	20	20.2	25	16	Q96R75	Q96R75 homo sapien
146	21	21.2	25	12	Q86951	Q86951 human herpe	219	20	20.2	25	4	Q9UCW4	Q9UCW4 homo sapien
147	21	21.2	25	13	Q9PS48	Q9ps48 crotalus at	220	20	20.2	25	17	Q9HBD7	Q9HBD7 homo sapien
148	21	21.2	25	15	Q91Q08	Q91qp8 human immun	221	20	20.2	25	10	Q9AUA5	Q9AUA5 arabis jacq
149	20.5	20.7	25	12	Q9J1I1	Q9j1i1 tt virus. o	222	20	20.2	25	17	Q9QV58	Q9QV58 mus sp. jac
150	20.5	20.7	25	12	Q9J1D7	Q9j1d7 tt virus. o	223	20	20.2	25	3	Q96V21	Q96V21 cryptococcu
151	20.5	20.7	25	12	Q9J1D7	Q9j1d7 tt virus. o	224	20	20.2	25	7	Q77923	Q77923 oreochromis
152	20.5	20.7	25	12	Q9J1D7	Q9j1d7 tt virus. o	225	20	20.2	25	18	Q82TX6	Q82TX6 pyrobaculum
153	20	20.2	10	11	Q9QV68	Q9qv68 mus sp. pro	226	20	20.2	25	19	Q9R4T9	Q9R4T9 bacillus th
154	20	20.2	13	10	Q9X1W6	Q9x1w6 oryza sativ	227	20	20.2	25	19	Q9S956	Q9S956 zea mays (m
155	20	20.2	14	2	P83077	P83077 bacillus ce	228	20	20.2	25	19	Q9OXP9	Q9OXP9 mus musculu
156	20	20.2	15	3	P82468	P82468 pseudomonas	229	20	20.2	25	19	Q9OXP9	Q9OXP9 gallus gall
157	20	20.2	15	3	Q96VH6	Q96vh6 penicillium	230	20	20.2	25	13	Q9PR59	Q9PR59 aeromonas h
158	20	20.2	15	12	Q66543	Q66543 human herpe	231	20	20.2	25	2	Q9KGR7	Q9KGR7 aeromonas h
159	20	20.2	16	4	Q9NNZ2	Q9nnz2 homo sapien	232	20	20.2	25	4	Q8WVL1	Q8WVL1 homo sapien
160	20	20.2	17	4	Q91L80	Q91l80 enterococcu	233	20	20.2	25	4	Q9UCR9	Q9UCR9 homo sapien
161	20	20.2	17	6	Q9TR05	Q9tr05 sus scrofa	234	20	20.2	25	4	Q9UCU1	Q9UCU1 homo sapien
162	20	20.2	18	9	Q9XU05	Q9xu05 bos taurus	235	20	20.2	25	10	Q9S8X5	Q9S8X5 glycine max
						Q9Xj95 bacterioph						Q9QVF9	Q9QVF9 rattus sp.

236	19	19.2	20	11	09QVB2	09QVB2 mus sp. ser	309	19	19.2	25	15	071994	071994 human immun
237	19	19.2	20	11	09QV28	09QV28 rattus sp.	310	19	19.2	25	15	072001	072001 human immun
238	19	19.2	20	12	084861	084861 unidentified	311	19	19.2	25	15	072006	072006 human immun
239	19	19.2	21	2	051540	051540 pseudomonas	312	19	19.2	25	15	072016	072016 human immun
240	19	19.2	21	2	09R414	09R414 helicobacter	313	19	19.2	25	15	072020	072020 human immun
241	19	19.2	21	4	09H4Z8	09H4Z8 homo sapien	314	19	19.2	25	15	0910P7	0910P7 human immun
242	19	19.2	21	6	09GJX3	09GJX3 sus scrofa	315	19	19.2	25	15	0910Q7	0910Q7 human immun
243	19	19.2	21	7	09S554	09S554 mus musculu	316	19	19.2	25	15	0910Q9	0910Q9 human immun
244	19	19.2	21	8	09TC76	09TC76 centropomus	317	18.5	18.7	21	5	024720	024720 drosophila
245	19	19.2	21	17	08RTG7	08RTG7 pyrococcus	318	18.5	18.7	25	5	09RW11	09RW11 aplysia cal
246	19	19.2	22	3	09SV26	09SV26 cryptococcu	319	18.5	18.7	25	11	P70382	P70382 mus musculu
247	19	19.2	22	3	09UR51	09UR51 cryptococcu	320	18	18.2	8	2	056140	056140 streptococ
248	19	19.2	22	6	097568	097568 sus scrofa	321	18	18.2	10	2	P83067	P83067 bacillus ce
249	19	19.2	22	11	088449	088449 rattus norv	322	18	18.2	10	3	09UVM2	09UVM2 schizophyl
250	19	19.2	22	12	089826	089826 murine minu	323	18	18.2	10	10	P82937	P82937 hordium vul
251	19	19.2	23	2	09S6S7	09S6S7 rhodobacter	324	18	18.2	10	11	09QV66	09QV66 mus sp. pro
252	19	19.2	23	3	096V17	096V17 cryptococcu	325	18	18.2	11	5	P83321	P83321 penaeus mon
253	19	19.2	23	3	096TMI	096TMI cryptococcu	326	18	18.2	11	11	099N81	099N81 mus musculu
254	19	19.2	23	4	016209	016209 homo sapien	327	18	18.2	12	2	09R7F1	09R7F1 staphylococ
255	19	19.2	23	4	09BS58	09BS58 homo sapien	328	18	18.2	13	2	P94878	P94878 lactococcus
256	19	19.2	23	4	096155	096155 homo sapien	329	18	18.2	14	2	08YU21	08YU21 streptococ
257	19	19.2	23	5	09TWU5	09TWU5 trichoplusi	330	18	18.2	14	4	015222	015222 homo sapien
258	19	19.2	23	10	09S8Q6	09S8Q6 spinacia ol	331	18	18.2	15	4	090C83	090C83 homo sapien
259	19	19.2	23	11	09CT97	09CT97 mus musculu	332	18	18.2	15	5	026323	026323 lymanaea sta
260	19	19.2	23	11	061948	061948 mus musculu	333	18	18.2	15	6	09YR89	09YR89 lymanaea sta
261	19	19.2	23	11	08RO71	08RO71 mus musculu	334	18	18.2	15	6	09YR45	09YR45 bos taurus
262	19	19.2	23	13	P70093	P70093 xenopus lae	335	18	18.2	15	9	09WBU7	09WBU7 vibrio phag
263	19	19.2	24	2	091720	091720 vibrio prot	336	18	18.2	15	10	P82430	P82430 nicotiana t
264	19	19.2	24	2	005124	005124 mycobacteri	337	18	18.2	15	11	09QVC4	09QVC4 rattus norv
265	19	19.2	24	2	09REB1	09REB1 escherichia	338	18	18.2	16	5	026322	026322 lymanaea sta
266	19	19.2	24	2	09R4B2	09R4B2 streptococ	339	18	18.2	16	6	095M79	095M79 equus cabal
267	19	19.2	24	2	053923	053923 streptomyce	340	18	18.2	16	8	09Y2C2	09Y2C2 nicotiana t
268	19	19.2	24	5	09TWU6	09TWU6 trichoplusi	341	18	18.2	16	10	P93232	P93232 lycopersico
269	19	19.2	24	10	093976	093976 gossypium h	342	18	18.2	16	10	09S8D6	09S8D6 triticum ae
270	19	19.2	24	10	09S8B4	09S8B4 lycopersico	343	18	18.2	16	10	P82453	P82453 spinacia ol
271	19	19.2	24	11	09S8A6	09S8A6 secale cere	344	18	18.2	17	4	09EUB3	09EUB3 cornebacte
272	19	19.2	24	11	089021	089021 mus musculu	345	18	18.2	17	4	016310	016310 homo sapien
273	19	19.2	25	11	09QV68	09QV68 rattus sp.	346	18	18.2	17	4	016073	016073 homo sapien
274	19	19.2	25	2	09WU14	09WU14 pseudomonas	347	18	18.2	17	10	09AUB2	09AUB2 arabidopsis
275	19	19.2	25	2	09EXB8	09EXB8 escherichia	348	18	18.2	17	10	09AUB9	09AUB9 lepidium ca
276	19	19.2	25	4	09UCR8	09UCR8 homo sapien	349	18	18.2	17	11	08QV56	08QV56 mus sp. fkb
277	19	19.2	25	4	09UCN7	09UCN7 homo sapien	350	18	18.2	17	12	085004	085004 porcine res
278	19	19.2	25	5	09UIG8	09UIG8 euploies oc	351	18	18.2	18	6	095N16	095N16 sorex arane
279	19	19.2	25	5	08SZG6	08SZG6 drosophila	352	18	18.2	19	2	087732	087732 streptomyce
280	19	19.2	25	9	09ZMW2	09ZMW2 bacteriopho	353	18	18.2	19	2	005601	005601 pseudomonas
281	19	19.2	25	10	039914	039914 gossypium r	354	18	18.2	19	2	09R524	09R524 clostridium
282	19	19.2	25	10	039915	039915 gossypium r	355	18	18.2	19	3	09ETP8	09ETP8 cryptococcu
283	19	19.2	25	10	P81643	P81643 emilliania h	356	18	18.2	19	3	096T11	096T11 cryptococcu
284	19	19.2	25	10	094199	094199 atropa bell	357	18	18.2	19	4	09UOG7	09UOG7 homo sapien
285	19	19.2	25	10	09S8V8	09S8V8 triticum ae	358	18	18.2	19	5	026321	026321 lymanaea sta
286	19	19.2	25	11	063464	063464 rattus norv	359	18	18.2	19	6	09YRK8	09YRK8 canis famli
287	19	19.2	25	11	09QV18	09QV18 mus sp. glu	360	18	18.2	19	10	0947Y4	0947Y4 oryza sativ
288	19	19.2	25	11	09QV22	09QV22 mus sp. 10-	361	18	18.2	19	10	011338	011338 moliuscum c
289	19	19.2	25	12	069148	069148 human herpe	362	18	18.2	19	12	090630	090630 baboon herp
290	19	19.2	25	13	091852	091852 xenopus lae	363	18	18.2	19	12	090633	090633 baboon herp
291	19	19.2	25	15	09DU42	09DU42 human immun	364	18	18.2	20	2	09R401	09R401 pseudomonas
292	19	19.2	25	15	099B06	099B06 human immun	365	18	18.2	20	3	096V30	096V30 cryptococcu
293	19	19.2	25	15	080273	080273 human immun	366	18	18.2	20	3	096TH5	096TH5 cryptococcu
294	19	19.2	25	15	071899	071899 human immun	367	18	18.2	20	3	012105	012105 rhizomucor
295	19	19.2	25	15	071906	071906 human immun	368	18	18.2	20	6	09YR84	09YR84 oryctolagus
296	19	19.2	25	15	071913	071913 human immun	369	18	18.2	20	6	09YR34	09YR34 ovis aries
297	19	19.2	25	15	071920	071920 human immun	370	18	18.2	20	6	09YR33	09YR33 canis famli
298	19	19.2	25	15	071927	071927 human immun	371	18	18.2	20	8	09Y214	09Y214 nicotiana s
299	19	19.2	25	15	071933	071933 human immun	372	18	18.2	20	10	P82163	P82163 spinacia ol
300	19	19.2	25	15	072010	072010 human immun	373	18	18.2	21	2	09X3C4	09X3C4 prochloroto
301	19	19.2	25	15	071876	071876 human immun	374	18	18.2	21	2	09R4D4	09R4D4 enterococcu
302	19	19.2	25	15	071882	071882 human immun	375	18	18.2	21	4	016218	016218 homo sapien
303	19	19.2	25	15	071887	071887 human immun	376	18	18.2	21	6	09YRV3	09YRV3 sus scrofa
304	19	19.2	25	15	071892	071892 human immun	377	18	18.2	21	13	09PS31	09PS31 elmeria ten
305	19	19.2	25	15	071969	071969 human immun	378	18	18.2	21	13	034297	034297 agrobacteri
306	19	19.2	25	15	071975	071975 human immun	379	18	18.2	22	2	P82580	P82580 streptococ
307	19	19.2	25	15	071981	071981 human immun	380	18	18.2	22	3	096T10	096T10 cryptococcu
308	19	19.2	25	15	071988	071988 human immun	381	18	18.2	22	3	096T10	096T10 cryptococcu

382	18	18.2	22	4	Q96C75	Q96C75 homo sapien	455	18	18.2	25	2	Q9RAE3	Q9RAE3 escherichia
383	18	18.2	22	6	Q9TRY5	Q9TRY5 sus sp. ins	456	18	18.2	25	2	Q9R386	Q9R386 yersinia ps
384	18	18.2	22	8	Q9MSX9	Q9MSX9 arctium lap	457	18	18.2	25	3	Q96V10	Q96V10 cryptococcu
385	18	18.2	22	8	Q9MSX7	Q9MSX7 clisium vul	458	18	18.2	25	4	Q9UED3	Q9UED3 homo sapien
386	18	18.2	22	8	Q9MSX6	Q9MSX6 cousinia hy	459	18	18.2	25	7	Q19452	Q19452 mus sapien
387	18	18.2	22	8	Q9MSX4	Q9MSX4 cynara humi	460	18	18.2	25	7	Q9T213	Q9T213 mus musculu
388	18	18.2	22	8	Q9MSX3	Q9MSX3 echinops sp	461	18	18.2	25	12	Q9PX08	Q9PX08 foot-and-mo
389	18	18.2	22	8	Q9MSX2	Q9MSX2 galactiles	462	18	18.2	25	12	Q96944	Q96944 human herpe
390	18	18.2	22	8	Q9MSW9	Q9MSW9 notodpasia s	463	18	18.2	25	12	Q86945	Q86945 human herpe
391	18	18.2	22	8	Q9MSW9	Q9MSW9 onopordum s	464	18	18.2	25	12	Q86947	Q86947 human herpe
392	18	18.2	22	8	Q9MSW8	Q9MSW8 onopordum ac	465	18	18.2	25	15	Q9T006	Q9T006 human herpe
393	18	18.2	22	8	Q9MSW6	Q9MSW6 silybum mar	466	18	18.2	25	2	Q52033	Q52033 human immun
394	18	18.2	22	8	Q9MSW5	Q9MSW5 tyrinum le	467	17.5	17.7	21	11	Q924H1	Q924H1 mus musculu
395	18	18.2	22	10	Q9XG00	Q9XG00 oryza sativ	468	17.5	17.7	23	10	Q9T2R3	Q9T2R3 pseudomonas
396	18	18.2	22	10	P81572	P81572 spinacia ol	469	17.5	17.7	25	10	Q9T2R3	Q9T2R3 solanum tub
397	18	18.2	22	10	Q9S899	Q9S899 pinus monti	470	17	17.2	8	6	Q9XSY1	Q9XSY1 arbidopsi
398	18	18.2	22	11	Q9CVJ5	Q9CVJ5 mus musculu	471	17	17.2	9	4	Q9H522	Q9H522 canis fami
399	18	18.2	22	16	Q9KAT7	Q9KAT7 bacillus ha	472	17	17.2	9	11	Q61723	Q61723 homo sapien
400	18	18.2	23	2	Q9R4T0	Q9R4T0 bordetella	473	17	17.2	9	12	Q92766	Q92766 mus musculu
401	18	18.2	23	2	Q9R570	Q9R570 nltrosomona	474	17	17.2	11	3	Q9UR95	Q9UR95 canine dist
402	18	18.2	23	3	Q96TM9	Q96TM9 cryptococcu	475	17	17.2	11	4	Q60614	Q9UR95 pichia angu
403	18	18.2	23	3	Q96TR8	Q96TR8 cryptococcu	476	17	17.2	11	4	P82436	Q60614 homo sapien
404	18	18.2	23	4	Q9UCR4	Q9UCR4 homo sapien	477	17	17.2	11	10	P82436	P82436 nicotiana t
405	18	18.2	23	4	Q16312	Q16312 homo sapien	478	17	17.2	12	2	Q9T4M9	Q9T4M9 streptococc
406	18	18.2	23	4	Q9UC00	Q9UC00 homo sapien	479	17	17.2	12	6	Q9TRT8	Q9TRT8 bos taurus
407	18	18.2	23	4	Q9UC09	Q9UC09 homo sapien	480	17	17.2	12	10	Q9SYT4	Q9SYT4 arbidopsi
408	18	18.2	23	6	Q9TR07	Q9TR07 canis fami	481	17	17.2	12	11	Q61331	Q61331 mus musculu
409	18	18.2	23	8	Q9MSX5	Q9MSX5 cynara card	482	17	17.2	13	4	Q9T2U1	Q9T2U1 bos sapien
410	18	18.2	23	8	Q8SLH1	Q8SLH1 taraxacum (	483	17	17.2	14	2	Q56945	Q56945 yersinia ps
411	18	18.2	23	8	Q8SLH0	Q8SLH0 taraxacum (	484	17	17.2	14	2	P81715	P81715 streptomyc
412	18	18.2	23	12	Q84331	Q84331 simian virtu	485	17	17.2	14	4	Q9UCS5	Q9UCS5 homo sapien
413	18	18.2	23	12	Q86946	Q86946 human herpe	486	17	17.2	14	10	Q9SAP8	Q9SAP8 pisum sativ
414	18	18.2	23	12	Q86948	Q86948 human herpe	487	17	17.2	14	12	P87540	P87540 barley mild
415	18	18.2	23	12	Q9YYM1	Q9YYM1 border dise	488	17	17.2	14	13	P70007	P70007 xenopus lae
416	18	18.2	23	12	Q9YYM0	Q9YYM0 border dise	489	17	17.2	14	15	Q10226	Q10226 human immun
417	18	18.2	23	12	Q9YYL9	Q9YYL9 border dise	490	17	17.2	14	15	Q10227	Q10227 human immun
418	18	18.2	23	12	Q9YYL7	Q9YYL7 border dise	491	17	17.2	14	15	Q10228	Q10228 human immun
419	18	18.2	23	12	Q9YYL6	Q9YYL6 border dise	492	17	17.2	14	15	Q10232	Q10232 human immun
420	18	18.2	23	12	Q9YYL5	Q9YYL5 border dise	493	17	17.2	14	15	Q10233	Q10233 human immun
421	18	18.2	23	12	Q9YYL4	Q9YYL4 border dise	494	17	17.2	14	15	Q10234	Q10234 human immun
422	18	18.2	23	12	Q9YYL3	Q9YYL3 border dise	495	17	17.2	15	2	Q9X635	Q9X635 escherichia
423	18	18.2	23	12	Q9YYL2	Q9YYL2 border dise	496	17	17.2	15	2	Q9X637	Q9X637 klebsiella
424	18	18.2	23	12	Q9YYL1	Q9YYL1 border dise	497	17	17.2	15	2	P83069	P83069 bacillus ce
425	18	18.2	23	12	Q9YYL0	Q9YYL0 border dise	498	17	17.2	15	4	Q9Y429	Q9Y429 homo sapien
426	18	18.2	23	12	Q9YYK9	Q9YYK9 border dise	499	17	17.2	15	4	Q9UEW3	Q9UEW3 homo sapien
427	18	18.2	23	12	Q9YYK8	Q9YYK8 border dise	500	17	17.2	15	4	Q9UE41	Q9UE41 homo sapien
428	18	18.2	23	12	Q9YYK7	Q9YYK7 border dise	501	17	17.2	15	4	Q9UCU5	Q9UCU5 homo sapien
429	18	18.2	23	13	Q13029	Q13029 boreogadus	502	17	17.2	15	5	Q9TWS0	Q9TWS0 pyura stolo
430	18	18.2	23	15	Q9EBS7	Q9EBS7 human immun	503	17	17.2	15	6	Q9TRP2	Q9TRP2 sus scrofa
431	18	18.2	23	15	Q99DB8	Q99DB8 human immun	504	17	17.2	15	6	Q9TRN4	Q9TRN4 sus scrofa
432	18	18.2	23	17	Q82ZN4	Q82ZN4 human immun	505	17	17.2	15	13	Q9PRW3	Q9PRW3 crocalus at
433	18	18.2	24	2	Q9EUI9	Q9EUI9 streptococc	506	17	17.2	15	13	Q9PRM3	Q9PRM3 gallus gall
434	18	18.2	24	2	Q9KIL6	Q9KIL6 pseudomonas	507	17	17.2	16	1	Q9UW44	Q9UW44 pyrococcus
435	18	18.2	24	2	Q9Z3Y9	Q9Z3Y9 pseudomonas	508	17	17.2	16	2	Q9LAP2	Q9LAP2 enterococcu
436	18	18.2	24	2	P81151	P81151 desulfovibrio	509	17	17.2	16	2	Q9R5E4	Q9R5E4 aeromonas h
437	18	18.2	24	4	Q9HB12	Q9HB12 homo sapien	510	17	17.2	16	2	Q9R596	Q9R596 micrococcus
438	18	18.2	24	5	Q26249	Q26249 drosophila	511	17	17.2	16	2	Q99374	Q99374 staphylococ
439	18	18.2	24	5	Q44050	Q44050 trypanosoma	512	17	17.2	16	4	Q99898	Q99898 homo sapien
440	18	18.2	24	5	Q24619	Q24619 drosophila	513	17	17.2	16	6	Q9TR09	Q9TR09 sus scrofa
441	18	18.2	24	5	Q9G0T1	Q9G0T1 rosa moscha	514	17	17.2	16	6	Q9TR75	Q9TR75 solanum tub
442	18	18.2	24	8	Q9G0T0	Q9G0T0 rosa phoeni	515	17	17.2	16	10	Q9S8N2	Q9S8N2 nicotiana t
443	18	18.2	24	8	Q9TIF2	Q9TIF2 lophostemon	516	17	17.2	16	11	Q54894	Q54894 mus musculu
444	18	18.2	24	8	Q9THL4	Q9THL4 myrtaceae g	517	17	17.2	16	11	Q9ERF8	Q9ERF8 ratius norv
445	18	18.2	24	8	Q9TIF0	Q9TIF0 eucalyptops	518	17	17.2	16	12	P90290	P90290 barley mild
446	18	18.2	24	8	Q9TIF5	Q9TIF5 arillastrum	519	17	17.2	17	2	Q9X515	Q9X515 enterococcu
447	18	18.2	24	8	Q9TIF5	Q9TIF5 eucalyptus	520	17	17.2	17	2	Q8VME2	Q8VME2 pseudomonas
448	18	18.2	24	8	Q9TIF5	Q9TIF5 eucalyptus	521	17	17.2	17	2	Q9RAV9	Q9RAV9 alcaligenes
449	18	18.2	24	8	Q9TIF5	Q9TIF5 eucalyptus	522	17	17.2	17	2	Q9W421	Q9W421 enterococcu
450	18	18.2	24	8	Q9GFW8	Q9GFW8 rosa gallic	523	17	17.2	17	2	Q9W420	Q9W420 enterococcu
451	18	18.2	24	8	Q9GFW7	Q9GFW7 rosa hybrid	524	17	17.2	17	6	Q18774	Q18774 crytocolagus
452	18	18.2	24	8	Q9MSX8	Q9MSX8 carduus nut	525	17	17.2	17	6	Q9SK07	Q9SK07 sus scrofa
453	18	18.2	25	2	Q45672	Q45672 bacillus su	526	17	17.2	17	7	Q9TNO0	Q9TNO0 mus sp. bet
454	18	18.2	25	2	Q9RAE2	Q9RAE2 escherichia	527	17	17.2	17	8	Q9T2S0	Q9T2S0 solanum tub

528	17	17.2	17	11	0920M0	0920M0 rattus norv	601	17	17.2	21	2	09X3K5	09X3K5 prochloroco
529	17	17.2	17	15	0783J24	0783J24 human immun	602	17	17.2	21	2	09X3K9	09X3K9 prochloroco
530	17	17.2	17	15	0783J26	0783J26 human immun	603	17	17.2	21	2	09X3L4	09X3L4 prochloroco
531	17	17.2	18	2	09ZF30	09ZF30 salmonella	604	17	17.2	21	2	09X3L8	09X3L8 prochloroco
532	17	17.2	18	2	08RL15	08RL15 neisseria m	605	17	17.2	21	2	09X3W5	09X3W5 prochloroco
533	17	17.2	18	3	001672	001672 pneumocysti	606	17	17.2	21	3	09UR89	09UR89 coccidioid
534	17	17.2	18	4	09UE43	09UE43 homo sapien	607	17	17.2	21	6	09SKS4	09SKS4 ovis aries
535	17	17.2	18	4	09UC58	09UC58 homo sapien	608	17	17.2	21	6	09SKA0	09SKA0 sus scrofa
536	17	17.2	18	5	09TWE0	09TWE0 biophalari	609	17	17.2	21	6	09TKT1	09TKT1 sus taurus
537	17	17.2	18	10	09S892	09S892 glycine max	610	17	17.2	21	6	09TKR1	09TKR1 sus taurus
538	17	17.2	18	10	09S818	09S818 oryza sativ	611	17	17.2	21	6	09TKR5	09TKR5 ovis aries
539	17	17.2	18	11	062532	062532 mus spreus	612	17	17.2	21	6	09TKR9	09TKR9 ursus arcto
540	17	17.2	18	13	090791	090791 gallus gall	613	17	17.2	21	15	078504	078504 human immun
541	17	17.2	18	13	09PSR6	09PSR6 struthio ca	614	17	17.2	22	15	078484	078484 human immun
542	17	17.2	19	2	09S6B1	09S6B1 streptomyce	615	17	17.2	22	2	09F0R2	09F0R2 staphylococ
543	17	17.2	19	3	09UR87	09UR87 candida par	616	17	17.2	22	2	09ZFR2	09ZFR2 enterobacte
544	17	17.2	19	4	099711	099711 homo sapien	617	17	17.2	22	6	09ZAW2	09ZAW2 francisella
545	17	17.2	19	5	09N654	09N654 drosophila	618	17	17.2	22	6	09ZAW2	09ZAW2 francisella
546	17	17.2	19	5	09N654	09N654 aedes aegyp	619	17	17.2	22	8	0957T4	0957T4 abies alba
547	17	17.2	19	5	09N654	09N654 aedes aegyp	620	17	17.2	22	10	09S897	09S897 citrus sine
548	17	17.2	19	6	09T8B6	09T8B6 clona intes	621	17	17.2	22	11	09J1D6	09J1D6 mesocricetu
549	17	17.2	19	10	09BDD6	09BDD6 ovis aries	622	17	17.2	22	15	09Q6G8	09Q6G8 human immun
550	17	17.2	19	10	043370	043370 allium cepa	623	17	17.2	22	15	09Q6G8	09Q6G8 human immun
551	17	17.2	19	10	09JCN8	09JCN8 oryza sativ	624	17	17.2	22	15	09Q6G2	09Q6G2 human immun
552	17	17.2	19	10	P82245	P82245 splinacia ol	625	17	17.2	22	15	09Q6G0	09Q6G0 human immun
553	17	17.2	19	11	09S8W5	09S8W5 avena sativ	626	17	17.2	22	15	09Q6F6	09Q6F6 human immun
554	17	17.2	19	11	09JK02	09JK02 mus musculu	627	17	17.2	22	15	09Q6F2	09Q6F2 human immun
555	17	17.2	19	12	09YR03	09YR03 porcine citr	628	17	17.2	22	15	09Q6E8	09Q6E8 human immun
556	17	17.2	19	12	09YR05	09YR05 porcine citr	629	17	17.2	22	15	09Q6E8	09Q6E8 human immun
557	17	17.2	19	12	09YR05	09YR05 porcine citr	630	17	17.2	22	15	09Q6E8	09Q6E8 human immun
558	17	17.2	19	12	09YR05	09YR05 porcine citr	631	17	17.2	22	15	09Q6E8	09Q6E8 human immun
559	17	17.2	19	12	056132	056132 porcine citr	632	17	17.2	22	15	09Q6E8	09Q6E8 human immun
560	17	17.2	19	13	09PRN4	09PRN4 porcine citr	633	17	17.2	22	15	09Q6E8	09Q6E8 human immun
561	17	17.2	19	15	09ORG9	09ORG9 petromyzon	634	17	17.2	22	15	09Q6E8	09Q6E8 human immun
562	17	17.2	20	2	09X629	09X629 human immun	635	17	17.2	22	15	09Q6E8	09Q6E8 human immun
563	17	17.2	20	2	09X630	09X630 unidentified	636	17	17.2	22	15	09Q6E8	09Q6E8 human immun
564	17	17.2	20	2	09X632	09X632 leclercia a	637	17	17.2	22	15	09Q6E8	09Q6E8 human immun
565	17	17.2	20	2	09X634	09X634 pseudomonas	638	17	17.2	22	15	09Q6E8	09Q6E8 human immun
566	17	17.2	20	2	050089	050089 seirratia ma	639	17	17.2	22	15	09Q6E8	09Q6E8 human immun
567	17	17.2	20	2	046499	046499 mycobacteri	640	17	17.2	22	15	09Q6E8	09Q6E8 human immun
568	17	17.2	20	4	09NWU7	09NWU7 desulfivibr	641	17	17.2	22	15	09Q6E8	09Q6E8 human immun
569	17	17.2	20	4	09NRC4	09NRC4 escherichia	642	17	17.2	22	15	09Q6E8	09Q6E8 human immun
570	17	17.2	20	4	09BRP3	09BRP3 homo sapien	643	17	17.2	22	15	09Q6E8	09Q6E8 human immun
571	17	17.2	20	4	08WM61	08WM61 homo sapien	644	17	17.2	22	15	09Q6E8	09Q6E8 human immun
572	17	17.2	20	4	09UC40	09UC40 homo sapien	645	17	17.2	22	15	09Q6E8	09Q6E8 human immun
573	17	17.2	20	5	08WX06	08WX06 homo sapien	646	17	17.2	22	15	09Q6E8	09Q6E8 human immun
574	17	17.2	20	5	09TWL2	09TWL2 octopus vul	647	17	17.2	22	15	09Q6E8	09Q6E8 human immun
575	17	17.2	20	5	09U8N5	09U8N5 scapomyza	648	17	17.2	22	15	09Q6E8	09Q6E8 human immun
576	17	17.2	20	5	09U8N2	09U8N2 scapomyza	649	17	17.2	22	15	09Q6E8	09Q6E8 human immun
577	17	17.2	20	6	09U8M9	09U8M9 scapomyza	650	17	17.2	22	15	09Q6E8	09Q6E8 human immun
578	17	17.2	20	6	028079	028079 bos taurus	651	17	17.2	22	15	09Q6E8	09Q6E8 human immun
579	17	17.2	20	7	019685	019685 homo sapien	652	17	17.2	22	15	09Q6E8	09Q6E8 human immun
580	17	17.2	20	11	09ET00	09ET00 mus musculu	653	17	17.2	22	15	09Q6E8	09Q6E8 human immun
581	17	17.2	20	11	09OVH4	09OVH4 rattus sp.	654	17	17.2	22	15	09Q6E8	09Q6E8 human immun
582	17	17.2	20	11	09QUT8	09QUT8 rattus sp.	655	17	17.2	22	15	09Q6E8	09Q6E8 human immun
583	17	17.2	20	11	09QUT8	09QUT8 rattus sp.	656	17	17.2	22	15	09Q6E8	09Q6E8 human immun
584	17	17.2	20	11	08RAP6	08RAP6 mus musculu	657	17	17.2	22	15	09Q6E8	09Q6E8 human immun
585	17	17.2	20	11	08RI17	08RI17 mus musculu	658	17	17.2	22	15	09Q6E8	09Q6E8 human immun
586	17	17.2	20	12	036978	036978 human papil	659	17	17.2	22	15	09Q6E8	09Q6E8 human immun
587	17	17.2	20	12	08V9H3	08V9H3 chicken ane	660	17	17.2	22	15	09Q6E8	09Q6E8 human immun
588	17	17.2	20	12	08UXT4	08UXT4 hepatitis c	661	17	17.2	22	15	09Q6E8	09Q6E8 human immun
589	17	17.2	20	12	08UXT3	08UXT3 hepatitis c	662	17	17.2	22	15	09Q6E8	09Q6E8 human immun
590	17	17.2	20	12	08UXT2	08UXT2 hepatitis c	663	17	17.2	22	15	09Q6E8	09Q6E8 human immun
591	17	17.2	20	12	08UXT1	08UXT1 hepatitis c	664	17	17.2	22	15	09Q6E8	09Q6E8 human immun
592	17	17.2	20	12	08UXT0	08UXT0 hepatitis c	665	17	17.2	22	15	09Q6E8	09Q6E8 human immun
593	17	17.2	20	12	08UXS9	08UXS9 hepatitis c	666	17	17.2	22	15	09Q6E8	09Q6E8 human immun
594	17	17.2	20	12	08UXS6	08UXS6 hepatitis c	667	17	17.2	22	15	09Q6E8	09Q6E8 human immun
595	17	17.2	20	12	08UXS5	08UXS5 hepatitis c	668	17	17.2	22	15	09Q6E8	09Q6E8 human immun
596	17	17.2	20	12	08UXS4	08UXS4 hepatitis c	669	17	17.2	22	15	09Q6E8	09Q6E8 human immun
597	17	17.2	20	12	08UXS3	08UXS3 hepatitis c	670	17	17.2	22	15	09Q6E8	09Q6E8 human immun
598	17	17.2	20	12	08UXS2	08UXS2 hepatitis c	671	17	17.2	22	15	09Q6E8	09Q6E8 human immun
599	17	17.2	20	12	08UXS1	08UXS1 hepatitis c	672	17	17.2	22	15	09Q6E8	09Q6E8 human immun
600	17	17.2	21	2	09X3F7	09X3F7 foot-and-mo	673	17	17.2	22	15	09Q6E8	09Q6E8 human immun

674	17	17.2	25	12	086943	086943 human herpe	747	16	16.2	17	12	085719	085719 reovirus (t
675	17	17.2	25	12	091061	091061 influenza a	748	16	16.2	17	12	0919B0	0919B0 human papil
676	17	17.2	25	12	091059	091059 influenza a	749	16	16.2	17	13	09DFB5	09dfb5 brachydanio
677	17	17.2	25	13	09YH56	09yh56 coturnix co	750	16	16.2	17	15	078328	078328 human immun
678	17	17.2	25	15	09WRES	09wres human immun	751	16	16.2	17	15	078345	078345 human immun
679	17	17.2	25	15	080E38	080e38 human immun	752	16	16.2	17	16	09K704	09k704 bacillus ha
680	17	17.2	25	15	080E33	080e33 human immun	753	16	16.2	18	2	09R584	09r584 rhodobacter
681	17	17.2	25	15	080E27	080e27 human immun	754	16	16.2	18	4	09H113	09h113 homo sapien
682	17	17.2	25	15	080E21	080e21 human immun	755	16	16.2	18	4	014042	014042 homo sapien
683	16.5	16.7	25	2	09RBS9	09rbs9 pseudomonas	756	16	16.2	18	4	096F98	096f98 homo sapien
684	16	16.2	9	4	09UCQ9	09ucq9 homo sapien	757	16	16.2	18	6	09GKH1	09gkh1 macaca mula
685	16	16.2	9	4	016220	016220 homo sapien	758	16	16.2	18	11	08VDM2	08vdm2 mus musculus
686	16	16.2	9	13	092009	092009 gallus gall	759	16	16.2	18	11	09IN55	09in55 polymaviru
687	16	16.2	10	11	090VE7	090ve7 rattus sp.	760	16	16.2	18	12	0919D5	0919d5 human papil
688	16	16.2	11	5	082698	082698 leucophaea	761	16	16.2	18	12	0919D3	0919d3 human papil
689	16	16.2	11	7	077892	077892 oreochromis	762	16	16.2	18	12	0919D1	0919d1 human papil
690	16	16.2	11	7	077906	077906 oreochromis	763	16	16.2	18	12	0919C9	0919c9 human papil
691	16	16.2	11	7	077918	077918 pseudotroph	764	16	16.2	18	12	0919C7	0919c7 human papil
692	16	16.2	11	12	040974	040974 cauliflower	765	16	16.2	18	12	0919C5	0919c5 human papil
693	16	16.2	12	4	09UC29	09uc29 homo sapien	766	16	16.2	18	12	0919B7	0919b7 human papil
694	16	16.2	12	13	069232	069232 bovine herp	767	16	16.2	18	12	0919B9	0919b9 human papil
695	16	16.2	12	13	090E13	090e13 xenopus lae	768	16	16.2	18	12	0919B7	0919b7 human papil
696	16	16.2	13	2	09RRT7	09rrt7 actinobacil	769	16	16.2	18	12	0919B5	0919b5 human papil
697	16	16.2	13	2	0936V1	0936v1 pseudomonas	770	16	16.2	18	12	0919B3	0919b3 human papil
698	16	16.2	13	4	09NR93	09nr93 homo sapien	771	16	16.2	18	12	0919A8	0919a8 human papil
699	16	16.2	14	4	09NY40	09ny40 homo sapien	772	16	16.2	18	15	087589	087589 chimpanzee
700	16	16.2	14	4	096062	096062 homo sapien	773	16	16.2	18	15	087591	087591 chimpanzee
701	16	16.2	14	5	P82209	P82209 bombyx mori	774	16	16.2	18	15	087593	087593 chimpanzee
702	16	16.2	14	10	09EYTO	09eyto allium cepa	775	16	16.2	19	1	09UWR8	09uwr8
703	16	16.2	14	10	094IT6	094it6 fragaria nu	776	16	16.2	19	2	09R2F7	09r2f7 escherichia
704	16	16.2	14	10	P82327	P82327 pisum sativ	777	16	16.2	19	2	09R4B9	09r4b9 streptococ
705	16	16.2	14	11	061864	061864 mus musculu	778	16	16.2	19	2	09R5C8	09r5c8 pseudomonas
706	16	16.2	14	12	085662	085662 reovirus (t	779	16	16.2	19	3	09R4X3	09r4x3 bacillus ce
707	16	16.2	14	12	084708	084708 porcine epi	780	16	16.2	19	3	092321	092321 saccharomyc
708	16	16.2	14	15	010231	010231 human immun	781	16	16.2	19	4	095598	095598 homo sapien
709	16	16.2	15	2	09R544	09r544 mycobacteri	782	16	16.2	19	4	09UC11	09uc11 homo sapien
710	16	16.2	15	8	09T2H9	09t2h9 nicotiana s	783	16	16.2	19	4	09UDB7	09udb7 homo sapien
711	16	16.2	15	9	038574	038574 bacterioph	784	16	16.2	19	5	09TWJ7	09twj7 mytilus edu
712	16	16.2	15	10	09S8Q8	09s8q8 ricinus com	785	16	16.2	19	6	019107	019107 bos taurus
713	16	16.2	15	11	090XZ5	090xz5 mus musculu	786	16	16.2	19	11	09S8G6	09s8g6 colocasia e
714	16	16.2	15	13	09PS10	09ps10 gallus gall	787	16	16.2	19	11	09CR60	09cr60 mus musculu
715	16	16.2	16	2	050900	050900 shigella so	788	16	16.2	19	12	086050	086050 human herpe
716	16	16.2	16	3	09UR86	09ur86 candida par	789	16	16.2	19	13	09D821	09d821 gallus gall
717	16	16.2	16	4	09UD47	09ud47 homo sapien	790	16	16.2	19	13	091433	091433 gallus gall
718	16	16.2	16	5	018378	018378 drosophila	791	16	16.2	19	13	042416	042416 gallus gall
719	16	16.2	16	6	077491	077491 nycticebus	792	16	16.2	19	13	091983	091983 gallus gall
720	16	16.2	16	6	09TRK9	09trk9 canis famill	793	16	16.2	19	15	091N44	091n44 human immun
721	16	16.2	16	6	09TS05	09ts05 bos taurus	794	16	16.2	19	15	085728	085728 spleen necr
722	16	16.2	16	6	09TRR5	09trr5 bos taurus	795	16	16.2	19	15	0905K4	0905k4 human immun
723	16	16.2	16	6	09TRH0	09trh0 bos taurus	796	16	16.2	19	15	0905K0	0905k0 human immun
724	16	16.2	16	6	09T2Q4	09t2q4 brassica na	797	16	16.2	19	15	0905H6	0905h6 human immun
725	16	16.2	16	8	08SL50	08sl50 aconitum mas	798	16	16.2	19	15	0905G4	0905g4 human immun
726	16	16.2	16	10	P83187	P83187 basella alb	799	16	16.2	20	1	09UWJ3	09uwj3 pyrococcus
727	16	16.2	16	11	090UM5	090um5 rattus sp.	800	16	16.2	20	2	09R896	09r896 chlamydia t
728	16	16.2	16	12	084246	084246 polymaviru	801	16	16.2	20	2	P72423	P72423 saccharopol
729	16	16.2	16	12	0919C3	0919c3 human papil	802	16	16.2	20	2	09R5R7	09r5r7 mycobacteri
730	16	16.2	16	13	09PSL6	09psl6 gallus gall	803	16	16.2	20	2	09R500	09r500 streptomyc
731	16	16.2	17	1	09UWLO	09uwlo pyrococcus	804	16	16.2	20	2	09R4F4	09r4f4 streptomys h
732	16	16.2	17	2	092G32	092g32 chlamydia t	805	16	16.2	20	2	09R4C7	09r4c7 mycobacteri
733	16	16.2	17	2	09R4H9	09r4h9 bordetella	806	16	16.2	20	2	09R4S0	09r4s0 mycobacteri
734	16	16.2	17	3	09C0S9	09c0s9 claviiceps p	807	16	16.2	20	2	09R4P2	09r4p2 brevundimon
735	16	16.2	17	3	09C0S8	09c0s8 claviiceps p	808	16	16.2	20	2	09R4U6	09r4u6 pseudomonas
736	16	16.2	17	3	09C0S7	09c0s7 claviiceps s	809	16	16.2	20	4	060696	060696 homo sapien
737	16	16.2	17	3	09C0S6	09c0s6 claviiceps a	810	16	16.2	20	4	09UC20	09uc20 homo sapien
738	16	16.2	17	3	09C1O8	09c1o8 claviiceps f	811	16	16.2	20	5	09U2M0	09u2m0 caenorhabdi
739	16	16.2	17	3	096T04	096t04 diaportha p	812	16	16.2	20	5	P82310	P82310 panulirus f
740	16	16.2	17	3	094758	094758 sclerotinia	813	16	16.2	20	6	09TRR7	09trr7 canis famill
741	16	16.2	17	4	09UC89	09uc89 homo sapien	814	16	16.2	20	6	09TRR5	09trr5 ovis aries
742	16	16.2	17	5	09TWPF	09twpf artemia (br	815	16	16.2	20	10	P83186	P83186 basella alb
743	16	16.2	17	6	09SM49	09sm49 bos taurus	816	16	16.2	20	10	09S900	09s900 vigna sinen
744	16	16.2	17	8	09T0Z5	09t0z5 macaca fasc	817	16	16.2	20	10	09S8U6	09s8u6 triticum ae
745	16	16.2	17	8	09T5Z9	09t5z9 pinelodelia	818	16	16.2	20	10	09S8U1	09s8u1 trichosanthe
746	16	16.2	17	10	065345	065345 gossypium h	819	16	16.2	20	10	09S8H8	09s8h8 brassica na

820	16	16.2	20	11	090U8	09qu8 mus sp. c-m	893	16	16.2	24	8	037804	037804 iris chryso
821	16	16.2	20	13	09PR3	09pr3 petromyzon	894	16	16.2	24	8	037829	037829 iris harte
822	16	16.2	20	13	09PS14	09ps14 oncorhynch	895	16	16.2	24	8	037824	037824 iris doula
823	16	16.2	21	2	09UP8	09jp8 iacobacill	896	16	16.2	24	8	032467	032467 iris purdyi
824	16	16.2	21	3	09RSE0	09rse0 aeromonas h	897	16	16.2	24	8	032458	032458 iris innoti
825	16	16.2	21	3	09UTR6	09utr6 schizosacch	898	16	16.2	24	10	039759	039759 gossypium a
826	16	16.2	21	4	015965	015965 homo sapien	899	16	16.2	24	10	P82139	P82139 spiniacia ol
827	16	16.2	21	4	0968P6	0968p6 homo sapien	900	16	16.2	24	10	042505	042505 gossypium a
828	16	16.2	21	4	09UC16	09uc16 homo sapien	901	16	16.2	24	10	039918	039918 gossypium r
829	16	16.2	21	6	09N0J5	09n0j5 saguinus lm	902	16	16.2	24	10	09S8G5	09s8g5 oryza sativ
830	16	16.2	21	8	09TRC8	09trc8 cornitermes	903	16	16.2	24	11	08R2H8	08r2h8 mus musculu
831	16	16.2	21	8	08SL63	08sl63 aeonium cas	904	16	16.2	24	13	09PSS9	09pss9 gallus gall
832	16	16.2	21	8	08SL47	08sl47 aeonium per	905	16	16.2	24	15	073766	073766 human immun
833	16	16.2	21	9	064183	064183 bacterioph	906	16	16.2	24	16	09K8M1	09k8m1 bacillus ha
834	16	16.2	21	11	P70657	P70657 rattus sp.	907	16	16.2	25	9	09NBE2	09nbe2 chironomus
835	16	16.2	21	12	09UG23	09jg23 lt virus. o	908	16	16.2	25	9	09FRZ2	09frz2 bacterioph
836	16	16.2	21	12	09UG30	09jg30 lt virus. o	909	16	16.2	25	10	040971	040971 pinus radia
837	16	16.2	21	13	09PSR6	09psr6 gallus gall	910	16	16.2	25	10	09S8R4	09s8r4 nicotiana t
838	16	16.2	21	13	09PRO1	09prq1 oncorhynch	911	16	16.2	25	11	064135	064135 mus sp. cal
839	16	16.2	21	15	082392	082392 human t-cel	912	16	16.2	25	11	060839	060839 mus musculu
840	16	16.2	21	15	082410	082410 human t-cel	913	16	16.2	25	11	091XN8	091xn8 rattus norv
841	16	16.2	21	15	082411	082411 human t-cel	914	16	16.2	25	11	090V49	090v49 rattus sp.
842	16	16.2	21	15	082412	082412 human t-cel	915	16	16.2	25	11	064341	064341 mus musculu
843	16	16.2	21	16	031871	031871 bacillus su	916	16	16.2	25	12	011472	011472 hepatitis c
844	16	16.2	22	2	093A12	093a12 thioabacillu	917	16	16.2	25	13	P82875	P82875 rana clamit
845	16	16.2	22	4	08W08	08w08 saccharomyc	918	16	16.2	25	15	09DU36	09du36 human immun
846	16	16.2	22	4	08W08	08w08 homo sapien	919	16	16.2	25	15	09DU28	09du28 human immun
847	16	16.2	22	4	09B224	09b224 homo sapien	920	16	16.2	25	15	09DU17	09du17 human immun
848	16	16.2	22	6	09N1W5	09n1w5 equus cabal	921	16	16.2	25	15	09S8T5	09s8t5 human immun
849	16	16.2	22	6	09TRB7	09trb7 bos taurus	922	16	16.2	25	15	09S8S6	09s8s6 human immun
850	16	16.2	22	8	037142	037142 artemia par	923	16	16.2	25	15	09S8S2	09s8s2 human immun
851	16	16.2	22	8	09TX1	09tx1 spiniacia ol	924	16	16.2	25	15	09S8R8	09s8r8 human immun
852	16	16.2	22	8	09TX28	09tx28 nicotiana t	925	16	16.2	25	15	09S8R3	09s8r3 human immun
853	16	16.2	22	10	09FPD9	09fpd9 hevea brasl	926	16	16.2	25	15	09S8R0	09s8r0 human immun
854	16	16.2	22	11	09QV15	09qv15 mus sp. syn	927	16	16.2	25	15	09S8B3	09s8b3 human immun
855	16	16.2	22	11	09QV59	09qv59 cavia (guin	928	16	16.2	25	15	09S8B0	09s8b0 human immun
856	16	16.2	22	11	08R487	08r487 rattus norv	929	16	16.2	25	15	09S8P7	09s8p7 human immun
857	16	16.2	22	12	084172	084172 of virus.	930	16	16.2	25	15	09S8P3	09s8p3 human immun
858	16	16.2	22	12	064831	064831 human adeno	931	16	16.2	25	15	09S8B0	09s8b0 human immun
859	16	16.2	22	13	0910C6	0910c6 gallinula c	932	16	16.2	25	15	09S8M8	09s8m8 human immun
860	16	16.2	22	13	090ZV4	090zv4 rallus liml	933	16	16.2	25	15	09S8L1	09s8l1 human immun
861	16	16.2	22	13	090ZV3	090zv3 rallus long	934	16	16.2	25	15	09S8K7	09s8k7 human immun
862	16	16.2	22	13	090ZV2	090zv2 sarothura	935	16	16.2	25	15	09S8T7	09s8t7 human immun
863	16	16.2	22	15	P89772	P89772 human immun	936	16	16.2	25	15	09S8T5	09s8t5 human immun
864	16	16.2	23	2	09S580	09s580 pseudomonas	937	16	16.2	25	15	0910O5	0910o5 human immun
865	16	16.2	23	2	086455	086455 pseudomonas	938	16	16.2	25	16	08X3Y0	08x3y0 escherichia
866	16	16.2	23	2	086987	086987 proteus mir	939	16	16.2	25	17	08ZYY5	08zyy5 pyrobaculum
867	16	16.2	23	2	054956	054956 spirulina p	940	15.5	15.7	20	4	09DMT8	09dm8 homo sapien
868	16	16.2	23	2	051776	051776 escherichia	941	15.5	15.7	20	13	09PRV5	09prv5 xenopus lae
869	16	16.2	23	4	09UC22	09uc22 homo sapien	942	15.5	15.7	23	13	090759	090759 gallus gall
870	16	16.2	23	4	09UC80	09uc80 homo sapien	943	15.5	15.2	8	6	09GWM3	09gm3 lagenorhync
871	16	16.2	23	5	09H4Y9	09h4y9 homo sapien	944	15.5	15.2	8	7	09S213	09s213 cryotolagus
872	16	16.2	23	5	094781	094781 trypanosoma	945	15.5	15.2	8	7	094VA0	094va0 varanus sem
873	16	16.2	23	8	09MSH2	09msH2 sphagnum ca	946	15.5	15.2	8	11	060615	060615 mus musculu
874	16	16.2	23	8	09MSH1	09msH1 sphagnum hyp	947	15.5	15.2	9	2	04S852	04s852 clostridium
875	16	16.2	23	10	09S893	09s893 arachis hyp	948	15.5	15.2	9	4	09UKR6	09ukr6 homo sapien
876	16	16.2	23	15	08USW2	08usw2 human immun	949	15.5	15.2	9	4	09UC36	09uc36 homo sapien
877	16	16.2	23	16	024856	024856 helicobacte	950	15.5	15.2	9	4	09UC36	09uc36 homo sapien
878	16	16.2	24	2	09ZF21	09zf21 proteus vul	951	15.5	15.2	9	4	09BX14	09bx14 homo sapien
879	16	16.2	24	2	09R4H1	09r4h1 amycolatops	952	15.5	15.2	9	6	09GJY3	09gjy3 lagenorhync
880	16	16.2	24	2	08RL36	08rl36 burkholderi	953	15.5	15.2	9	6	09GJY2	09gjy2 lagenorhync
881	16	16.2	24	3	007140	007140 saccharomyc	954	15.5	15.2	9	6	09GJY1	09gjy1 lagenorhync
882	16	16.2	24	4	09BUC0	09buc0 homo sapien	955	15.5	15.2	9	6	09TT77	09tt77 bos taurus
883	16	16.2	24	4	08WYB9	08wyb9 homo sapien	956	15.5	15.2	9	11	008979	008979 mus musculu
884	16	16.2	24	5	09BM10	09bm10 spongilla l	957	15.5	15.2	9	12	P90359	P90359 barley mild
885	16	16.2	24	5	P82204	P82204 bombyx mori	958	15.5	15.2	10	2	08RSU1	08rsu1 helicobacte
886	16	16.2	24	7	09S9R2	09s9r2 drosophila	959	15.5	15.2	10	5	026093	026093 pisaster oc
887	16	16.2	24	7	078181	078181 homo sapien	960	15.5	15.2	10	5	P82223	P82223 bombyx mori
888	16	16.2	24	8	032444	032444 iris bracte	961	15.5	15.2	10	11	P82224	P82224 bombyx mori
889	16	16.2	24	8	032452	032452 iris fernal	962	15.5	15.2	10	11	090V99	090v99 mus sp. pro
890	16	16.2	24	8	032459	032459 iris macros	963	15.5	15.2	10	13	090Y93	090y93 gallus gall
891	16	16.2	24	8	032471	032471 iris tenuis	964	15.5	15.2	11	2	09LAF7	09laf7 bacillus ce
892	16	16.2	24	8	037085	037085 iris tenax	965	15.5	15.2	11	4	09UC04	09uc04 homo sapien

966	15	15.2	11	4	Q9UCU3	Q9UCU3 homo sapien
967	15	15.2	11	5	Q9TWM2	Q9TWM2 aplysia cal
968	15	15.2	11	5	Q26092	Q26092 plaister oc
969	15	15.2	11	11	Q9Z1H5	Q9Z1H5 mus musculi
970	15	15.2	12	2	Q053J8	Q053J8 sphingomona
971	15	15.2	12	2	Q47251	Q47251 escherichia
972	15	15.2	12	2	Q9RS57	Q9RS57 helicobacte
973	15	15.2	12	2	Q9RS55	Q9RS55 helicobacte
974	15	15.2	12	4	Q13865	Q13865 homo sapien
975	15	15.2	12	5	Q26429	Q26429 drosophila
976	15	15.2	12	6	Q9XS31	Q9XS31 sus scrofa
977	15	15.2	12	8	Q8SL49	Q8SL49 aeoniu lan
978	15	15.2	12	8	Q8SL40	Q8SL40 aeoniu urb
979	15	15.2	13	2	Q9RE12	Q9RE12 acidiphiliu
980	15	15.2	13	4	Q9UEP7	Q9UEP7 homo sapien
981	15	15.2	13	4	Q99931	Q99931 homo sapien
982	15	15.2	13	4	Q9UCS4	Q9UCS4 homo sapien
983	15	15.2	13	8	Q9T569	Q9T569 zea mays (m
984	15	15.2	13	12	Q65331	Q65331 autographa
985	15	15.2	13	13	P83009	P83009 lamna nasu
986	15	15.2	14	2	Q9R7M3	Q9R7M3 bacillus st
987	15	15.2	14	2	Q85576	Q85576 chlamydia t
988	15	15.2	14	2	Q46291	Q46291 canadian pe
989	15	15.2	14	2	Q56750	Q56750 western x p
990	15	15.2	14	6	Q09061	Q09061 bos taurus
991	15	15.2	14	8	Q9T2K7	Q9T2K7 chlamydomon
992	15	15.2	14	10	P83222	P83222 pisum sativi
993	15	15.2	14	10	Q852V1	Q852V1 zea mays (f
994	15	15.2	14	12	Q9W982	Q9W982 hepaticu c
995	15	15.2	14	12	Q9PY99	Q9PY99 murine hepi
996	15	15.2	15	2	Q9RAD6	Q9RAD6 escherichia
997	15	15.2	15	2	Q9R547	Q9R547 mycobacteri
998	15	15.2	15	2	Q9RS34	Q9RS34 pseudomonas
999	15	15.2	15	2	Q9RS51	Q9RS51 micrococcu
1000	15	15.2	15	4	Q9U51	Q9U51 homo sapien

## ALIGNMENTS

RESULT 1	ID	ORGXUI	PRELIMINARY:	PRT:	24 AA.
AC	ORGXUI;				
DT	01-MAR-2002 (TReMBLrel. 20, Created)				
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)				
DT	01-MAR-2002 (TReMBLrel. 20, Last annotation update)				
DT	BC12-associated X protein (Fragment).				
DT	BAX.				
DS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Thorncroft E.C., Schwartzfarb E.M., Manfredi J.J.;				
RT	"A conserved intronic response element mediates direct p53-dependent				
RL	transcriptional activation of both the human and murine bax genes."				
DR	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.				
FT	EMBL; AF39054; AAL73333.1; -				
FT	NCN_TER 24 24				
SO	SEQUENCE 24 AA; 2379 MW; 8C3D3BB7479B798 CRC64;				
Query Match		31.3%;	Score 31;	DB 4;	Length 24;
Best Local Similarity		40.0%;	Pred. No. 3e+02;		
Matches	6; Conservative		4; Mismatches	5; Indels	0; Gaps

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OY      4 CHERMGRGRTSSKEL 18
         | : | | | | : :
Db      5 GEQPRGGGPTSSQI 19
```

## RESULT 2

ID	015912	PRELIMINARY;	PRT;	18 AA.
AC	015912:			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, last sequence update)		
DT	01-MAR-2002	(TREMBLrel. 20, last annotation update)		
DE	zinc finger homeodomain protein (Fragment).			
GN	ARZF1-B.			
OC	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LUNG;			
RX	MEDLINE=96070776; PubMed=7592926;			
RA	Miura Y., Tam T., Ido A., Morinaga T., Miki T., Hashimoto T.,			
RA	Tamaoki T.;			
RT	"Cloning and characterization of an ATBF1 isoform that expresses in a			
RT	neuronal differentiation-dependent manner.";			
RL	J. Biol. Chem. 270:26840-26846(1995).			
DR	EMBL; L32833; AAC37582.1; -.			
KW	DNA-binding; Homeobox; Nuclear protein.			
FT	NON_TER			
SO	SEQUENCE			
	18 AA; 1960 MW; 5176F62C445BE7DE CRC64;			
Query Match	29.3%;	Score 29;	DB 4;	length 18;
Best Local Similarity	50.0%;	Pred. No. 4.9e+02;		
Matches	6;	Conservative	3;	Mismatches 3; Indels 0; Gaps 0;
OY	7 RMGRGRITSSKEL 18			
	! ! ! ! ! ! ! ! ! !			
db	2 RUGGGGLVSEEL 13			

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QY 7 RMGRGRTSSKEL 18
    |::|: |::|
Db 2 RLGGGQLVSEEL 13
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RESULT 3	
Q9M7J2	
ID Q9M7J2	PRELIMINARY;
Q9M7J2	PRT; 23 AA

DT	01-OCT-2000	(TIREMBLrel. 15, Created)
DT	01-OCT-2000	(TIREMBLrel. 15, Last sequence update)
DT	01-MAR-2002	(TIREMBLrel. 20, Last annotation update)
DE	Tamadas 51-like protein (Fragment).	
OS	Hordeum chilense x Triticum durum.	
OC	Eudaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;	
OC	Triticeae; Hordeum x Triticum.	
OX	NCBI_TaxId=49967;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-H7174;	
RA	Salgueiro S., Gil J., Steele S.H., Savazzini F., Riley A.,	
RA	Lazzeri P.A., Barcelo P.;	
RT	"Sequence of part of a cereal MADS-box gene promoter.";	
RL	Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.	
DR	EMBL; AF132736; AAF29592.1;	
DR	InterPro; IPR002100; TF_MADSbox.	
DR	Pfam; PF00319; SRF-TE; 1.	
DR	SMART; SM00432; MADS; 1.	
DR	PROSITE; PSS0066; MADS_BOX_2; 1.	
FT	NON_TER	23
FT	NON_TER	23
SQ	SEQUENCE	23 AA; 2723 MW; 7499F79B5D424418 CRC64;
Query Match		
Best Match	Similarity	28.3%; Score 28; DB 10; Length 23;
Matches	5; Conservative	45.5%; Pred. No. 9.3e+02;
	2; Mismatches	4; Indels
		0; Gaps
		0;

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QY      8 MGRGRTSSKEL 18
        ||||: | :
Db      1 MGRGKIEIKRI 11
```

## RESULT 4



Q922R1 PRELIMINARY; PRT; 23 AA.  
 ID Q922R1  
 AC Q922R1  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Histone H2A (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 NCBI\_TaxID=10116;  
 RX MEDLINE=94452395; PubMed=10524764;  
 RA Chai Y.C.; Chae C.B.;  
 RT "DNA hypomethylation and germ cell-specific expression of testis-  
 specific H2B histone gene";  
 RL Thesis (1992), University of North Carolina at Chapel Hill.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Chai Y.C.;  
 RT "The genomic and sequence analysis of rat histone H2B genes.";  
 RL DNA Seq. 9:353-358(1998).  
 DR EMBL: AF032898; AAC98916.1; -  
 FT NON\_TER  
 SQ SEQUENCE 23 AA; 2417 MW; CBEFFC323632794E CRC64;

Query Match 28.3%; Score 28; DB 11; Length 23;  
 Best Local Similarity 38.5%; Pred. No. 9.3e+02;  
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 GHERMGRGRTSSK 16  
 ID 1 : 1 : 1111:  
 DB 8 GGRRAKAKTSSR 20

RESULT 5  
 Q13376 PRELIMINARY; PRT; 17 AA.  
 ID Q13376  
 AC Q13376  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE RNA Binding motif (Fragment).  
 GN RBM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RX MEDLINE=97032533; PubMed=8875892;  
 RA Prosser J., Ingalls J.D., Condie A., Ma K., Kerr S., Thakrar R.,  
 RT Taylor K., Cameron J.M., Cooke H.J.;  
 RT "Degeneracy in human multiplicity RBM (YRRM), a candidate spermatogenesis  
 gene.";  
 RL Mamm. Genome 7:835-842(1996).  
 DR EMBL: U38450; AAB49815.1; -  
 FT NON\_TER  
 SQ SEQUENCE 17 AA; 2060 MW; 98CDD6AEFFC350012 CRC64;

Query Match 27.3%; Score 27; DB 4; Length 17;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGRGTS 14  
 ID 1 : 1 : 1111:  
 DB 3 GGRGSS 8

RESULT 6  
 Q9DEH9 PRELIMINARY; PRT; 20 AA.  
 ID Q9DEH9

AC Q9DEH9;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE MCM4 (Fragment).  
 GN MCM4.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NCBI\_TaxID=8355;  
 RX MEDLINE=20456723; PubMed=11003390;  
 RA Fujimori A., Ataki R., Fukumura R., Ohnata T., Takahashi H.,  
 RA Kawahara A., Tatsumi K., Abe M.;  
 RT "Identification of four highly conserved regions in DNA-PKcs.";  
 RL Immunogenetics 51:965-973(2000).  
 DR EMBL: AB016729; BAB19264.1; -  
 FT NON\_TER  
 SQ SEQUENCE 20 AA; 2247 MW; 7F3A0A50B30441AB CRC64;

Query Match 27.3%; Score 27; DB 13; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 1.2e+03;  
 Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 NVPGHERMGRGRTS 14  
 ID 1 : 1 : 1111:  
 DB 6 STPSRRNRKGRGS 19

RESULT 7  
 Q9GFA0 PRELIMINARY; PRT; 24 AA.  
 ID Q9GFA0  
 AC Q9GFA0  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Photosystem II subunit (Fragment).  
 GN PSBH.  
 OS Calycanthus floridus (Sweet shrub).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Laurales; Calycanthaceae; Calycanthus.  
 NCBI\_TaxID=3429;  
 RX MEDLINE=11080123; PubMed=11080123;  
 RA Graham S.W., Olmstead R.G.;  
 RT "Utility of 17 chloroplast genes for inferring the phylogeny of the  
 RT basal angiosperms.";  
 RL Am. J. Bot. 87:1712-1730(2000).  
 DR EMBL: AF123846; AAG26264.1; -  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 24 AA; 2562 MW; F04BAD0139E57A11 CRC64;

Query Match 27.3%; Score 27; DB 8; Length 24;  
 Best Local Similarity 41.2%; Pred. No. 1.4e+03;  
 Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 VPGHERMGRGRTSSKEL 18  
 ID 1 : 1 : 1111:  
 DB 6 VEGSSRSRGPRTTLTGDL 22

RESULT 8  
 Q905H2 PRELIMINARY; PRT; 19 AA.  
 ID Q905H2  
 AC Q905H2  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Fat protein (Fragment).  
 OS Human immunodeficiency virus type 1  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97CG275;  
 RA Taniguchi Y., Takeshita J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
 RA Ichimura H., Parra H.-J.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vif/vif Sequences in  
 RT Republic of Congo-Brazzaville";  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF410446; AAL10250.1;  
 FT NON\_TER 1 1  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2290 MW; 366296E191128236 CRC64;

Query Match 26.3%; Score 26; DB 15; Length 19;  
 Best Local Similarity 45.5%; Pred. No. 1.7e+03;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 7 RMGRGRTSSKE 17  
 DB 1 RGRGRTSSKE 11

## RESULT 9

GOBYRO 09DYRO PRELIMINARY; PRT; 20 AA.  
 ID 09DYRO:  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE Gag polyprotein (Fragment).  
 GN Gag.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20461476; PubMed=11005867;  
 RA Martinez-Ficado J., Depasquale M.P., Kartsonis N., Hanna G.J.,  
 RA Wong J., Finzi D., Rosenberg E., Guntard H.F., Sutton L., Savara A.,  
 RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,  
 RA Siliciano R., D'Aquila R.T.;  
 RT "Antiretroviral resistance during successful therapy of HIV type 1  
 RT infection";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).  
 DR EMBL; AF292884; AAG25530.1;  
 FT NON\_TER 1 1  
 FT NON\_TER 1 1  
 SQ SEQUENCE 20 AA; 2436 MW; CODEC0F60E8539F CRC64;

Query Match 26.3%; Score 26; DB 15; Length 20;  
 Best Local Similarity 45.5%; Pred. No. 1.8e+03;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 8 MGRGRTSSKE 18  
 DB 9 MWGRTPNERL 19

## RESULT 10

GOBYRO 09R573 PRELIMINARY; PRT; 24 AA.  
 ID 09R573:  
 AC 09R573:  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
 DE Hydroxylamine oxidoreductase (Fragment).  
 OS Nitrosomonas europaea.

OC Bacteria; Proteobacteria; beta subdivision;  
 OC Ammonia-oxidizing bacteria; Nitrosomonas.  
 OX NCBI\_TaxID=915;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=93315429; PubMed=8325841;  
 RA Arciero D.M., Hooper A.B.;  
 RT "Hydroxylamine oxidoreductase from Nitrosomonas europaea is a multimer  
 RT of an octa-heme subunit";  
 RL J. Biol. Chem. 268:14645-14654(1993).  
 DR HSSP: 050925; IRGI.  
 SQ SEQUENCE 24 AA; 2663 MW; 7EC6594C5DC0D9D64 CRC64;

Query Match 26.3%; Score 26; DB 2; Length 24;  
 Best Local Similarity 36.4%; Pred. No. 2.1e+03;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 7 RMGRGRTSSKE 17  
 DB 14 KIDRGKATPKE 24

## RESULT 11

GOBYRO 09G6T8 PRELIMINARY; PRT; 24 AA.  
 ID 09G6T8:  
 AC 09G6T8:  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Unknown (Protein for IMAGE:4025108) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SKIN;  
 RA Strausberg R.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC009233; AAH09233.1;  
 FT NON\_TER 1 1  
 FT NON\_TER 1 1  
 SQ SEQUENCE 24 AA; 2698 MW; 1870BFBA387E7A CRC64;

Query Match 26.3%; Score 26; DB 4; Length 24;  
 Best Local Similarity 62.5%; Pred. No. 2.1e+03;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 GRTSSKE 18  
 DB 11 GRPASREL 18

## RESULT 12

GOBYRO 08VHY7 PRELIMINARY; PRT; 24 AA.  
 ID 08VHY7:  
 AC 08VHY7:  
 DT 01-MAR-2002 (TReMBLrel. 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Bcl2-associated X protein (Fragment).  
 GN BAX.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RA Thorburn E.C., Schwartzfarb E.M., Manfredi J.J.;  
 RT "A conserved intronic response element mediates direct p53-dependent  
 RT transcriptional activation of both the human and murine bax genes";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF339055; AAL73334.1;

FT NON\_TER 24 24  
SQ SEQUENCE 24 AA: 2326 MW: 998C7EBB7479A6CC CRC64;

Query Match 26.3%; Score 26; DB 11; Length 24;  
Best Local Similarity 41.7%; Pred. No. 2.1e+03;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 6 ERMGRTSSKE 17  
|:|:|:|:|  
Db 6 EOLSGGPTSS 17

## RESULT 13

ID 09R763 PRELIMINARY; PRT: 19 AA.

AC 09R763; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
CP60-1 protein (Fragment).

OC Rhizobium leguminosarum (biovar viciae).

CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OX NCBI\_TaxID=387;

RN [1]

RP SEQUENCE FROM N.A.

RC SPRAIN-VICIAE;

RA Wallington E.J., Smart D., Downie J.A., Lund P.A.;

RT "Distinct modes of regulation in two of the three chaparron operons of Rhizobium leguminosarum."

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: Y12483; CAA73087.1; -.

FT NON\_TER 19 19

SQ SEQUENCE 19 AA: 2196 MW: B046232A25C67C41 CRC64;

OY 4 CHERMGRC 11  
|:|:|:|

Db 12 GREKMLRG 19

## RESULT 14

ID 016271 PRELIMINARY; PRT: 19 AA.

AC 016271; 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
Arginine vasopressin V2 receptor (Fragment).

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Holtzman E.J., Kolakowski L.F., Jr., Gelfman-Holtzman O., O'Brien D.G.,

RT "Mutations in the vasopressin V2 receptor gene in two families with nephrogenic diabetes insipidus."

DR J. Am. Soc. Nephrol. 5:165-176(1994).

FT NON\_TER 1 1

SQ SEQUENCE 19 AA: 1905 MW: 181640EFD90F2788 CRC64;

Query Match 25.3%; Score 25; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPCH 5  
|:|:|

Db 1 VPCH 4

## RESULT 15

ID 085658 PRELIMINARY; PRT: 19 AA.

AC 085658; 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
Reovirus serotype 2 L3 (Fragment).

OS Reovirus (type 2 / strain D5/Jones).

CC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.

OX NCBI\_TaxID=10885;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-83017877; PubMed-7123853;

RA Galliard R.K., Li J.K., Keene J.D., Joklik W.K.;

RT "The sequences at the termini of four genes of the three reovirus serotypes."

RL Virology 121:320-326(1982).

DR EMBL: J02305; AAA47244.1; -.

FT NON\_TER 19 19

SQ SEQUENCE 19 AA: 2103 MW: D61D8C331FD8BAEF CRC64;

OY 7 RMGGRTRSSK 16  
|:|:|:|

Db 6 KRTGKSSGK 15

## RESULT 16

ID 090UZO PRELIMINARY; PRT: 21 AA.

AC 090UZO; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
Alpha class glutathione S-transferase subunit 8 (EC 2.5.1.18) (Fragment).

OS Rattus sp.

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10118;

RN [1]

RP SEQUENCE

RA MEDLINE-96036981; PubMed-7485987;

RA Rouimi P., Debrauner L., Tuillier J.;

RT "Electrospray ionization-mass spectrometry as a tool for characterization of glutathione S-transferase isozymes."

DR Anal. Biochem. 229:304-312(1995).

DR HSSP: P24472; IGUK.

SQ SEQUENCE 21 AA: 2675 MW: AEA8DA961F24972C CRC64;

OY 9 GRGRTSS 15  
|:|:|:|

Db 12 GGRGMS 18

Query Match 25.3%; Score 25; DB 11; Length 21;  
Best Local Similarity 71.4%; Pred. No. 2.7e+03;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## RESULT 17

ID 09DD39 PRELIMINARY; PRT: 21 AA.

AC 09DD39;

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DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Non-W chromodomain helicase DNA binding protein (W-linked chromodomain
DE helicase DNA binding protein) (Fragment).
GN NON-W CHD OR W-LINKED CHD.
OS Nipponia nippon.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Ciconiiformes; Threskiornithidae;
OC Nipponia.
OX NCBI_TaxID=128390;
RN [1]
RP SEQUENCE FROM N.A.
RA Arai Y., Ishii S., Kikuchi M.;
RT "Nipponia nippon non-W CHD gene."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Arai Y., Ishii S., Kikuchi M.;
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[2]
DR EMBL; AB049443; BAB15804.1; -.
DR EMBL; AB049444; BAB15805.1; -.
KW Helicase.
FT NON_TER 1 1
FT 21 21
SQ SEQUENCE 21 AA; 2588 MW; C8E13B3B1AD353E3 CRC64;

Query Match 25.3%; Score 25; DB 13; Length 21;
Best Local Similarity 41.7%; Pred. No. 2.7e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 ERMGRGRTSSKE 17
Db 8 KKGRRPTPIPRE 19
:::1111:1

RESULT 18
ID 057692 PRELIMINARY; PRT; 22 AA.
AC 057692;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE CHROMO-helicase-DNA-binding ON A NON-W chromosome protein (Fragment).
GN CHD OR CHD-W.
OS Otis tarda.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruliformes; Otididae; Otis.
OX NCBI_TaxID=73107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-016, AND D16;
RA Pitra C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047391; AAC04869.1; -.
DR EMBL; AF047390; AAC04868.1; -.
KW DNA-binding; Helicase.
FT NON_TER 1 1
FT 22 22
SQ SEQUENCE 22 AA; 2675 MW; C8E13B3B1ABA5573 CRC64;

Query Match 25.3%; Score 25; DB 13; Length 22;
Best Local Similarity 41.7%; Pred. No. 2.9e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 ERMGRGRTSSKE 17
Db 9 KKGRRPTPIPRE 20
:::1111:1

RESULT 19
Q99215
Q99215

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ID Q99215 PRELIMINARY; PRT; 25 AA.
AC Q99215;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
DE Albumin (Fragment).
OS Trilicium monococcum (Elkorn wheat) (Small spelt).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4568;
RN [1]
RP SEQUENCE.
RA Shewry P.R., Lafandra D., Salcedo G., Aragocillo C.;
RA Garcia-Olmedo F., Lew E.J.-L., Dietler M.D., Kasarda D.D.;
RL FEBS Lett. 175:359-363(1984).
DR HSSP; P01088; 1BRA.
KW Seed storage protein.
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2585 MW; DA1FA028621066F0 CRC64;

Query Match 25.3%; Score 25; DB 10; Length 25;
Best Local Similarity 43.8%; Pred. No. 3.3e+03;
Matches 7; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 2 VPG---HERMGRGT 13
Db 7 VPGGLMPHNPIGACRT 22
:::1111:1

RESULT 20
ID Q9UD45 PRELIMINARY; PRT; 16 AA.
AC Q9UD45;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Gamma-interferon (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95038487; Pubmed=7951030;
RA Smirnova O.Iu., Tat'kov S.I., Petrenko V.A., Il'ichev A.A.,
RA Sandakchiev L.S.;
RT "[Mutant human gamma-interferons with varied C-termini and their
RT properties].";
RL Dokl. Akad. Nauk 337:405-406(1994).
SQ SEQUENCE 16 AA; 2006 MW; 2CFED1938CCA84CB CRC64;

Query Match 24.2%; Score 24; DB 4; Length 16;
Best Local Similarity 45.5%; Pred. No. 3e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 ERMGRGRTSSK 16
Db 6 EMLFRGRRASQ 16
:::1111:1

RESULT 21
Q9R0J9 PRELIMINARY; PRT; 16 AA.
ID Q9R0J9;
AC Q9R0J9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Ras-GTPase-activating protein SH3-domain binding protein
DE (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitagawa Y., Nakamura K., Inoue K., Sakai T.;
RT "Rat ras-GTPase-activating protein SH3-domain binding protein.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032425; BAA84530.1;
FT NON_TER
SO SEQUENCE 16 AA; 1713 MW; 315DCERC3BB10AB4 CRC64;

Query Match 24.2%; Score 24; DB 11; Length 16;
Best Local Similarity 40.0%; Pred. No. 3e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 8 MGRGRTSSKE 17
Db 7 VGRGRTTPRO 16

RESULT 22
OY9Y973 PRELIMINARY; PRT; 17 AA.
AC OY9Y973;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG12485 protein.
GN CG12485.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phrygotea; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer J.R., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinelt K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

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RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003791; AAF57423.1;
DR FlyBase; FBgn0034547; CG12485.
SO SEQUENCE 17 AA; 1907 MW; 47D598D29F4860DE CRC64;

Query Match 24.2%; Score 24; DB 5; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 3 PGHERMGR 10
Db 10 PHHAQGR 17

RESULT 23
OY9AUB3 PRELIMINARY; PRT; 17 AA.
AC OY9AUB3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Chalcone synthase (Fragment).
OS Arabidopsis halleri subsp. halleri.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=81971;
RN [1]
RP SEQUENCE FROM N.A.
RA Koch M., Kroymann J., Haubold B., Weissshaar B., Mitchell-Olds T.;
RT "Phylogenetic analysis of promoter sequences from cruciferous
RT plants.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF248986; AAK31921.1;
FT NON_TER
SO SEQUENCE 17 AA; 1752 MW; 31D56C76CB0E40CE CRC64;

Query Match 24.2%; Score 24; DB 10; Length 17;
Best Local Similarity 45.5%; Pred. No. 3.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 8 MGRGRTSSKE 18
Db 3 MAGGASSSDEI 13

RESULT 24
OY9TRK3 PRELIMINARY; PRT; 19 AA.
AC OY9TRK3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 20, Last annotation update)
DE TCP-1 RING complex subunit P1 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=93099850; PubMed=1361170;
RA Frydman J., Nimmeggen E., Erdjument-Bromage H., Wall J.S., Tempst P.,
RA Hartl F.U.;
RT "Function in protein folding of Tric, a cytosolic ring complex
RT containing TCP-1 and structurally related subunits.";
RL EMBL J. 11:4767-4778(1992).
DR InterPro: IPR002493; Chaperonin-TCP-1.
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; cpn60_TCP1; 1.
DR PROSITE: PS00995; TCP1_3; 1.
KW ATP-binding; Chaperone.

```

SQ SEQUENCE 19 AA; 1906 MW; 844291D811086990 CRC64;

Query Match 24.2%; Score 24; DB 6; Length 19;

Best Local Similarity 42.9%; Pred. No. 3.6e+03;

Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 6 ERMGRGRTSSKELA 19  
: | | | | |  
Db 4 DEVGDGTTSTVTLA 17

RESULT 25

Q90RG1 PRELIMINARY; PRT; 19 AA.

AC Q90RG1; Q90RG1;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Tat protein (Fragment).

TAT.

Human immunodeficiency virus type 1.

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=97CG257;

RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,

RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,

RT Hayami M., Ichimura H., Parra J.H.,

RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in

RT Republic of Congo-Brazzaville."

RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF127549; AAK84910.1; -

FT NON\_TER 1 1

FT NON\_TER 19 19

SQ SEQUENCE 19 AA; 2261 MW; 3E4296F35E068236 CRC64;

Query Match 24.2%; Score 24; DB 15; Length 19;

Best Local Similarity 45.5%; Pred. No. 3.6e+03;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 RMGRGRTSSKE 17  
| | | | |  
Db 1 RQRRGTPSSRQ 11

Search completed: March 14, 2003, 16:07:12

Up time : 53 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:04:07 ; Search time 16 Seconds  
(without alignments)  
114.160 Million cell updates/sec

Title: US-09-674-913a-1

Perfect score: 99

Sequence: 1 NVPGERMGRGRTSSKELA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues 4984

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :  
1: PIR\_73:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	30.3	20	2	S48654
2	30	30.3	23	2	E39855
3	30	30.3	23	2	C39855
4	30	30.3	23	2	D39855
5	29	29.3	18	2	I53453
6	29	29.3	23	2	F39855
7	29	29.3	23	2	G39855
8	25	25.3	16	2	A31963
9	24	24.2	15	2	PL0143
10	24	24.2	16	2	PH0766
11	24	24.2	17	2	C30221
12	24	24.2	18	2	B24735
13	24	24.2	19	2	S28396
14	24	24.2	21	2	S29858
15	24	24.2	21	2	I50535
16	24	24.2	23	2	PC4030
17	24	24.2	24	2	S40666
18	23	23.7	16	2	S78415
19	23	23.2	15	2	JT0610
20	23	23.2	15	2	S36891
21	23	23.2	16	2	C45143
22	23	23.2	18	2	PS0387
23	23	23.2	22	2	I50533
24	23	23.2	23	2	I61239
25	23	23.2	24	2	I76886
26	22	22.2	13	2	S36668
27	22	22.2	16	2	H49037
28	22	22.2	17	2	A61334
29	22	22.2	20	2	E60894

30	22	22.2	21	2	B12055	glyceraldehyde-3-p
31	22	22.2	21	2	PT0227	Ig heavy chain CDK
32	22	22.2	21	2	C49042	Ig heavy chain V r
33	22	22.2	23	2	E54346	pyruvate synthase
34	22	22.2	23	2	S10448	nucleocapsid prote
35	22	22.2	23	2	G81890	hypothetical prote
36	22	22.2	23	2	S10609	dodecenoyl-CoA Del
37	22	22.2	25	2	A60842	somatostatin-25 -
38	21	21.2	11	2	PH0938	T-cell receptor be
39	21	21.2	12	2	PH0169	NADH2 dehydrogenas
40	21	21.2	11	2	T44420	hypothetical prote
41	21	21.2	14	2	C33098	223k exoantigen -
42	21	21.2	15	2	A38304	heterogeneous ribo
43	21	21.2	16	2	C49039	T-cell receptor be
44	21	21.2	16	2	JH0517	Insulin-like growt
45	21	21.2	18	1	MTDFBC	melanotropin beta
46	21	21.2	19	2	S31613	beta-1,3-glucanase
47	21	21.2	20	2	S14161	probable drp-4-ke
48	21	21.2	20	2	S03505	T-cell receptor al
49	21	21.2	21	2	S69371	duodenase - bovine
50	21	21.2	21	2	A60975	HMG1/2 homolog - a
51	21	21.2	22	2	B60475	glyceraldehyde-3-p
52	21	21.2	22	2	PT0070	hypothetical prote
53	21	21.2	22	2	C42856	hypothetical prote
54	21	21.2	23	2	S43765	ribosomal protein
55	21	21.2	23	2	S16363	opacity protein P.
56	21	21.2	23	2	B30988	hypothetical prote
57	21	21.2	24	2	PN0163	glyceraldehyde-3-p
58	21	21.2	24	2	A60606	Rhodopsin - Calfo
59	21	21.2	24	2	S53793	actin - mouse (fra
60	21	21.2	25	2	PC1119	atrolysin A (EC 3.
61	21	21.2	25	2	A34179	neuromedin U - com
62	21	21.2	25	2	S39391	calpain II heavy c
63	20.5	20.7	24	2	A41037	antimicrobial pept
64	20	20.2	7	2	A15398	choline oxidase (E
65	20	20.2	15	2	S02381	probable membrane
66	20	20.2	15	2	PN0052	pyruvate kinase (E
67	20	20.2	16	2	PH1771	T cell receptor al
68	20	20.2	18	2	B27504	histone H2B - mous
69	20	20.2	18	2	A35676	hypothetical prote
70	20	20.2	19	2	S16332	peroxidase (EC 1.1
71	20	20.2	19	2	C39305	neurotoxin Tx3 - s
72	20	20.2	20	2	A05332	serum amyloid P-co
73	20	20.2	20	2	A47687	3-dehydroquinatate d
74	20	20.2	20	2	S78759	ribosomal protein
75	20	20.2	21	2	S61410	pyruvate, phosphat
76	20	20.2	21	2	B49042	Ig heavy chain V r
77	20	20.2	22	2	A39269	LX-1 tumor antigen
78	20	20.2	23	2	A60423	monophenol monooxy
79	20	20.2	24	2	S59908	endothelial cell-v
80	20	20.2	25	2	S62673	glyceraldehyde-3-p
81	20	20.2	25	2	JP0047	ribosomal protein
82	20	20.2	25	2	UF0048	glial fibrillary a
83	20	20.2	25	2	A35734	chiorophyll a/b-bi
84	19.5	19.7	18	2	S13974	serine proteinase
85	19.5	19.7	20	2	PC2084	sodium channel III
86	19.5	19.7	23	2	A44824	somatostatin-25 -
87	19.5	19.7	25	2	B60840	H4 histone - Afric
88	19	19.2	6	2	IS1434	Ig heavy chain CRD
89	19	19.2	9	2	PT0324	T-cell receptor al
90	19	19.2	10	2	PT0213	NADH2 dehydrogenas
91	19	19.2	10	2	P00785	chemical-sense-rel
92	19	19.2	11	2	S65395	Em protein - wheat
93	19	19.2	12	2	S36902	6-phosphofructokin
94	19	19.2	12	2	S16204	Ig gamma-2b chain
95	19	19.2	12	2	C30503	T-cell receptor be
96	19	19.2	12	2	PH0931	myosin heavy chain
97	19	19.2	13	2	A23695	hypothetical prote
98	19	19.2	13	2	S52356	glyceraldehyde-3-p
99	19	19.2	13	2	S54344	cytochrome-c oxida
100	19	19.2	14	2	S65392	hypothetical prote
101	19	19.2	15	2	C37765	ribosomal protein
102	19	19.2	15	2	S36889	

103	19	19.2	15	2	PA0091	methionine adenosy	176	18	18.2	20	2	A40451	dormancy-related p
104	19	19.2	15	2	PH1342	Ig heavy chain DJ	177	18	18.2	20	2	PQ0684	photosystem I 15.9
105	19	19.2	15	2	A27504	histone H2A - mous	178	18	18.2	20	2	S19615	phobosin - polyhaet
106	19	19.2	17	2	A61321	histone H4 - commo	179	18	18.2	21	2	S12883	DNA gyrase chain A
107	19	19.2	17	2	B61321	histone H4 - chick	180	18	18.2	22	2	A61497	seed protein ws-12
108	19	19.2	17	2	B44923	carboxypeptidase 3	181	18	18.2	22	2	F23734	Insulin-like growt
109	19	19.2	17	2	A61211	anantin - Streptom	182	18	18.2	22	2	B35372	Identified low M
110	19	19.2	18	2	S23950	45K protein - pig	183	18	18.2	22	2	A37043	Ig light chain, po
111	19	19.2	17	2	PRO332	Ig heavy chain CRD	184	18	18.2	22	2	G83924	hypothetical prote
112	19	19.2	20	2	S68620	histone H4 - sea u	185	18	18.2	23	2	A39855	paralytic peptide
113	19	19.2	20	2	S06149	photosystem I chal	186	18	18.2	23	2	S13268	heat shock protein
114	19	19.2	20	2	A60365	trypsin inhibitor	187	18	18.2	23	2	E43253	nuclear antigen EB
115	19	19.2	20	2	S68617	histone H2A - sea	188	18	18.2	23	2	PX0070	nuclear antigen P3
116	19	19.2	20	2	A55899	basement membrane	189	18	18.2	23	2	A48845	sterol regulatory
117	19	19.2	20	2	S78419	ribosomal protein	190	18	18.2	24	2	F24406	unspecific monooxy
118	19	19.2	21	2	PN0082	sperm chromatin pr	191	18	18.2	24	2	S10601	dimethylalanine mo
119	19	19.2	21	2	A02903	alpha-crystallin c	192	18	18.2	24	2	PN0172	serine proteinase
120	19	19.2	22	2	S52357	hypothetical prote	193	18	18.2	24	2	S07645	hst-omega protein
121	19	19.2	23	2	S38738	lipid transfer pro	194	18	18.2	25	2	E37520	glutathione transf
122	19	19.2	23	2	I51431	histone H4-1 precu	195	18	18.2	25	2	PQ0683	photosystem I 16.1
123	19	19.2	23	2	I54773	neural cell adhesi	196	18	18.2	25	2	D49253	nuclear antigen EB
124	19	19.2	23	2	S72535	probable acr-2 reg	197	18	18.2	25	2	PRO287	Ig heavy chain CRD
125	19	19.2	24	2	A56631	paralytic peptide	198	17.5	17.7	20	2	D49164	chromogranin-B - r
126	19	19.2	24	2	B43295	histone H4 - alfal	199	17.5	17.7	22	2	S04228	N4-(beta-N-acetyl)
127	19	19.2	24	2	S53749	histone H4 - rat	200	17	17.2	5	2	PRO608	T-cell receptor be
128	19	19.2	24	2	JP0052	omega 1-40 secalin	201	17	17.2	7	2	E61491	angiotensin-conver
129	19	19.2	24	2	S70329	ada 3'-region alKB	202	17	17.2	8	2	A31570	seed protein ws-5
130	19	19.2	24	2	B39433	T-cell acute lymph	203	17	17.2	8	2	PRO279	Ig heavy chain CRD
131	19	19.2	24	2	I38253	protein-tyrosine k	204	17	17.2	9	2	E41978	calliIFMamide 5 -
132	19	19.2	25	2	I51565	cellulase (EC 3.2.	205	17	17.2	10	1	GMR012	leucosulfafakinin-II
133	19	19.2	25	2	A45920	histone H2B - sea	206	17	17.2	10	2	I60588	sperm-activating p
134	19	19.2	25	2	PS0145	ribosomal protein	207	17	17.2	10	2	B60656	leucosulfafakinin II
135	19	19.2	25	2	JP0045	rev protein - huma	208	17	17.2	10	2	A42089	transcription fact
136	19	19.2	25	2	T09385	coenzyme F420 hydr	209	17	17.2	10	2	B56899	serum heterodimer,
137	19	19.2	25	2	S63484	T-cell receptor J-	210	17	17.2	11	2	B24736	inhibin beta-B cha
138	19	19.2	25	2	S47190	CDK inhibitor - mo	211	17	17.2	11	1	GMR01	leucosulfafakinin -
139	19	19.2	25	2	S39360	kinase-related tra	212	17	17.2	11	2	PT0081	protein QA300023 -
140	18.5	18.7	23	2	A41263	Ig heavy chain CRD	213	17	17.2	11	2	A60656	perisulfafakinin - A
141	18	18.2	9	2	PRO246	fibriopeptide B -	214	17	17.2	12	2	PH1587	Ig H chain V-D-J r
142	18	18.2	9	2	S78420	ribosomal protein	215	17	17.2	13	1	MTCMAD	melanotropin alpha
143	18	18.2	9	2	S39437	D-amin-acid oxida	216	17	17.2	13	1	MTCH0D	melanotropin alpha
144	18	18.2	9	2	A26120	6-phosphofructokin	217	17	17.2	13	2	S57571	T-cell receptor al
145	18	18.2	11	2	S45698	gamma-MSH-like pro	218	17	17.2	13	2	S47358	T-cell antigen rec
146	18	18.2	11	2	C38887	T-cell receptor ga	219	17	17.2	14	2	I51430	hemoglobin beta ch
147	18	18.2	11	2	S34447	binr protein - Sta	220	17	17.2	14	2	I51432	histone H4-1 precu
148	18	18.2	12	2	S68402	NAD(+)-glycohydrol	221	17	17.2	14	2	A56632	neoesulfafakinin-II -
149	18	18.2	12	2	S33800	chaperone, TCP1-re	222	17	17.2	14	2	S36678	dococenoil-CoA Del
150	18	18.2	13	2	S23372	T-cell receptor al	223	17	17.2	15	2	S29878	Na+/K+-exchanging
151	18	18.2	13	2	PH1311	Ig heavy chain DJ	224	17	17.2	15	2	S13973	chlorophyll a/b-bi
152	18	18.2	14	2	PH1321	hemoglobin beta ch	225	17	17.2	15	2	PC2215	fibriogenolytic p
153	18	18.2	14	4	I52618	protein QF200007 -	226	17	17.2	15	2	A49480	major immunophilin
154	18	18.2	15	2	PA0055	urinary tract ston	227	17	17.2	16	2	PH1310	Ig heavy chain DJ
155	18	18.2	15	2	A61247	H+-transporting tw	228	17	17.2	16	2	S51735	T-cell receptor be
156	18	18.2	15	2	A56049	Ig heavy chain CDR	229	17	17.2	16	2	JN0264	translatin initia
157	18	18.2	16	2	PT0296	T-cell receptor be	230	17	17.2	16	2	PH1580	Ig H chain V-D-J r
158	18	18.2	16	2	H49039	calcium-binding pr	231	17	17.2	17	2	S20490	photosystem II chl
159	18	18.2	18	2	B34473	protein phosphatas	232	17	17.2	17	2	PH1357	Ig heavy chain DJ
160	18	18.2	18	2	A32917	orf21 5' of eryk -	233	17	17.2	17	2	PD0005	very-high-density
161	18	18.2	19	2	PC1324	hypothetical prote	234	17	17.2	17	2	AF2093	heterocyst-inhibit
162	18	18.2	19	2	PC1322	hypothetical prote	235	17	17.2	18	1	MTCH0B	melanotropin beta
163	18	18.2	19	2	A49254	Tcr delta chain V-	236	17	17.2	18	2	A36133	hypothetical prote
164	18	18.2	19	2	S65435	manganese peroxida	237	17	17.2	18	2	S70612	alpha-macroglobuli
165	18	18.2	19	2	S65435	calpain (Ec 3.4.22	238	17	17.2	18	2	S54272	CRC 75 protein - h
166	18	18.2	19	2	S65435	seed protein ws-25	239	17	17.2	18	2	S47196	T-cell receptor J-
167	18	18.2	20	2	G61491	ribosomal protein	240	17	17.2	18	2	I49408	cytochrome-c oxida
168	18	18.2	20	2	JPO055	densinal fluid tra	241	17	17.2	19	2	S20289	glutathione transf
169	18	18.2	20	2	DIRT	hypothetical prote	242	17	17.2	19	2	S32548	pepsin-like protei
170	18	18.2	20	2	S33001	GroEL protein homo	243	17	17.2	19	2	A92058	glycogen(starch) s
171	18	18.2	20	2	PC4385		244	17	17.2	19	2	S02269	
172	18	18.2	20	2	PC4386		245	17	17.2	19	2		
173	18	18.2	20	2			246	17	17.2	19	2		
174	18	18.2	20	2			247	17	17.2	19	2		
175	18	18.2	20	2			248	17	17.2	19	2		



249	17	17.2	19	2	S63485	coenzyme F420 hydr
250	17	17.2	19	2	S29212	protein C - cat (f
251	17	17.2	20	2	A39328	notch1s II-5b non
252	17	17.2	20	2	B61333	chymotrypsin (EC 3
253	17	17.2	20	2	A49164	chromogranin-B - r
254	17	17.2	20	2	S68619	histone H3 - sea u
255	17	17.2	20	2	E39419	collagen alpha 5(I
256	17	17.2	20	2	S00315	photosystem I chai
257	17	17.2	20	2	S63483	photosystem I chai
258	17	17.2	20	2	S63483	photosystem I chai
259	17	17.2	20	2	S57286	translational elonga
260	17	17.2	20	2	S06150	photosystem I chai
261	17	17.2	20	2	S19616	globin - polychaet
262	17	17.2	20	2	S53440	glutathione-binding
263	17	17.2	20	2	S43627	cytochrome-c oxida
264	17	17.2	20	2	I55663	MHC HLA-DR gamma
265	17	17.2	20	2	A41437	alpha-1-antiprotei
266	17	17.2	21	2	PC4387	GroEL protein homo
267	17	17.2	21	2	S33287	DNA polymerase - T
268	17	17.2	21	2	S47189	T-cell receptor J-
269	17	17.2	21	2	J02196	hypothetical 2.5k
270	17	17.2	21	2	A60684	L-ascorbate peroxi
271	17	17.2	21	2	S31427	biliary glycoprote
272	17	17.2	22	2	A20359	translational elonga
273	17	17.2	22	2	PH1359	Ig heavy chain DJ
274	17	17.2	22	2	S47195	T-cell receptor J-
275	17	17.2	22	2	A45913	plantaricin A - La
276	17	17.2	23	2	S21275	tryptase (EC 3.4.2
277	17	17.2	23	2	B45220	glia-activating fa
278	17	17.2	23	2	C56978	collagen alpha 1(I)
279	17	17.2	23	2	I55406	nicotinic acetylch
280	17	17.2	23	2	S16361	opacity protein P.
281	17	17.2	23	2	A56272	conjugation induc
282	17	17.2	23	4	S33889	hypothetical prote
283	17	17.2	24	1	JF0016	probable 2.9k prot
284	17	17.2	24	2	BMTD	bombinin - Bombina
285	17	17.2	24	2	S11384	thymidine phosphor
286	17	17.2	24	2	I46513	tropomyosin I - rabl
287	17	17.2	24	2	D53402	glut 5'-region con
288	17	17.2	24	2	PF0076	leucine dehydrogen
289	17	17.2	24	2	T07991	hypothetical prote
290	17	17.2	24	2	T08160	S locus-linked pro
291	17	17.2	24	2	S70333	endosperm protein,
292	17	17.2	25	2	S56003	glucan 1,3-beta-gl
293	17	17.2	25	2	A45109	chymotrypsin (EC 3
294	17	17.2	25	2	A23698	tryptase (EC 3.4.2
295	17	17.2	25	2	S10850	alpha-amylase inhi
296	17	17.2	25	2	A18864	enkephalin-contain
297	17	17.2	25	2	D41575	bombinin-like pept
298	17	17.2	25	2	JH0700	omega-conotoxin MV
299	17	17.2	25	2	S47204	T-cell receptor J-
300	17	17.2	25	2	S65729	hemoglobin, extrac
301	17	17.2	25	2	E41839	ribosomal protein
302	17	17.2	25	2	S77862	ribosomal protein
303	17	17.2	25	2	B65274	hypothetical prote
304	17	17.2	25	2	A23605	histone H1.1 - whe
305	17	17.2	25	2	A61499	glutathione transf
306	17	17.2	25	2	S03456	T-cell receptor al
307	17	17.2	25	2	PC4445	L-ascorbate peroxi
308	16.5	16.7	21	2	S56002	glucan 1,3-beta-gl
309	16.5	16.7	21	2	B29663	histone H2B - star
310	16.5	16.7	24	2	S47194	T-cell receptor J-
311	16.5	16.7	24	2	B42266	peptidylglycine mo
312	16	16.2	5	2	S34405	adenylate kinase (
313	16	16.2	8	2	PT0553	T-cell receptor be
314	16	16.2	8	2	T48890	hypothetical prote
315	16	16.2	9	2	PT0554	T-cell receptor be
316	16	16.2	9	2	B45020	probable minipolyp
317	16	16.2	9	2	B41983	orf downstream to b
318	16	16.2	9	2	I50633	c-rel protein - ch
319	16	16.2	9	2	S26508	collagen alpha 2(V
320	16	16.2	10	2	PC7078	unidentified 48.7k
321	16	16.2	10	2	S65388	cytochrome-c oxida
322	16	16.2	10	2	S24190	tryptase (EC 3.4.2
322	16	16.2	10	2	A37617	tirose-phosphate i
323	16	16.2	10	2	H37196	bradykinin-potentl
324	16	16.2	11	2	A14454	6-phosphofructokin
325	16	16.2	12	2	S26548	T-cell receptor be
326	16	16.2	12	2	S65629	protoporphyrinogen
327	16	16.2	12	2	S10626	lipovitellin - Afr
328	16	16.2	12	2	PR0228	Ig heavy chain CDR
329	16	16.2	12	2	PH1461	T-cell receptor be
330	16	16.2	13	1	XAV19B	angiotensin-conver
331	16	16.2	13	2	A32734	enkephalin precurs
332	16	16.2	13	2	S78519	ribosomal protein
333	16	16.2	13	2	D39690	neural cell adhesi
334	16	16.2	13	2	B58533	CD61 homoloig - cha
335	16	16.2	13	2	PR0331	Ig heavy chain CRD
336	16	16.2	13	2	PH0796	T-cell receptor al
337	16	16.2	13	2	PH0799	T-cell receptor al
338	16	16.2	13	2	PH0783	T-cell receptor al
339	16	16.2	14	2	S27140	hypothetical prote
340	16	16.2	14	2	PA0096	pyruvate decarboxy
341	16	16.2	14	2	E61308	hemocyanin chain 3
342	16	16.2	14	2	S43629	cytochrome-c oxida
343	16	16.2	14	2	I64815	carbonic anhydrase
344	16	16.2	14	2	PH1332	Ig heavy chain DJ
345	16	16.2	14	2	PH1322	Ig heavy chain DJ
346	16	16.2	14	2	E49039	T-cell receptor be
347	16	16.2	15	2	PR0681	photosystem I 19.0
348	16	16.2	15	2	C56979	collagen alpha 1(I
349	16	16.2	15	2	S36896	ribosomal protein
350	16	16.2	15	2	PA0018	photosystem I 9k P
351	16	16.2	15	2	S67975	apolipoprotein CB2
352	16	16.2	15	2	G41299	T-cell receptor al
353	16	16.2	15	2	B49655	T-cell-receptor be
354	16	16.2	15	2	B56978	collagen alpha 2(X
355	16	16.2	15	2	A53594	calnexin - mouse (
356	16	16.2	15	2	PH0775	T-cell receptor al
357	16	16.2	15	2	PH0779	T-cell receptor al
358	16	16.2	15	2	C44101	calmodulin, vasoac
359	16	16.2	15	4	I38336	melanotropin beta
360	16	16.2	16	1	MRP8S	casein Kinase II (
361	16	16.2	16	2	C45133	myosin light chain
362	16	16.2	16	2	A27803	fibrinopeptide A -
363	16	16.2	16	2	H29501	heat shock protein
364	16	16.2	16	2	C44896	hypothetical prote
365	16	16.2	16	2	S01104	leukocyte chemoatc
366	16	16.2	16	2	JM0609	T-cell receptor be
367	16	16.2	16	2	PH0773	vesiculatinin I - e
368	16	16.2	17	1	A61339	ribosomal protein
369	16	16.2	17	2	S17274	large granule L6 c
370	16	16.2	17	2	PC1318	T-cell receptor be
371	16	16.2	17	2	I24687	dihydrolipoamide S
372	16	16.2	17	2	A37823	enamelin, 26k - bo
373	16	16.2	17	2	S10786	hypothetical prote
374	16	16.2	17	2	C84063	translational elonga
375	16	16.2	18	2	S39153	ribosomal protein
376	16	16.2	18	2	S49026	protein P6f - gold
377	16	16.2	18	2	D59137	INS150A/INS150B mu
378	16	16.2	18	4	SA0064	Ig kappa chain V r
379	16	16.2	19	2	A28814	ubiquitin - Thermo
380	16	16.2	19	2	S34459	cytochrome c(EDH)
381	16	16.2	19	2	J29766	ribosomal protein
382	16	16.2	19	2	JP0057	hypothetical prote
383	16	16.2	19	2	S59717	globin - polychaet
384	16	16.2	19	2	A19613	cAMP-regulated pho
385	16	16.2	19	2	A13361	ribosomal protein
386	16	16.2	19	2	S78411	5-carboxymethyl-2-
387	16	16.2	20	2	B53875	creatin kinase (E
388	16	16.2	20	2	S00492	hemocyanin chain I
389	16	16.2	20	2	GM0492	gamma-crystallin (
390	16	16.2	20	2	CG1570	water-soluble 35k
391	16	16.2	20	2	JM0252	immunodeficiency v
392	16	16.2	20	2	S65399	homeotic protein H
393	16	16.2	20	2	I65242	pufk protein [limpo
394	16	16.2	20	2	T50757	

395	16	16.2	20	2	S71017	hypoethetical prote
396	16	16.2	20	2	P00046	citrate (sl)-synh
397	16	16.2	20	2	S32387	ribosomal protein
398	16	16.2	20	2	T26748	hypoethetical prote
399	16	16.2	20	2	A48406	annexin VI homolog
400	16	16.2	20	2	A60812	plasma proteolase
401	16	16.2	20	2	E54226	light-harvesting p
402	16	16.2	21	2	S25603	NADH2 dehydrogenas
403	16	16.2	21	2	A32521	hexokinase (EC 2.7
404	16	16.2	21	2	A38837	T-cell receptor be
405	16	16.2	21	2	PH1690	Ig heavy chain V r
406	16	16.2	21	2	E44101	calmodulin, vasoac
407	16	16.2	21	2	S28436	major outer membra
408	16	16.2	21	2	S39455	34K ribonucleoprot
409	16	16.2	21	2	C31182	hypoethetical 2.4K
410	16	16.2	21	2	S22875	tya protein - yeas
411	16	16.2	21	2	S62893	cold-Inducible pro
412	16	16.2	21	2	I54268	alpha-1-antichymot
413	16	16.2	21	2	B49200	cystatin-related p
414	16	16.2	21	2	I53263	CRP-1 delta - rat
415	16	16.2	21	2	T12935	hypoethetical prote
416	16	16.2	22	2	A26376	peptidyl-dipectida
417	16	16.2	22	2	B48395	probable angiotens
418	16	16.2	22	2	C38389	histone H2B - sea
419	16	16.2	22	2	B40288	chaperonin 10 - Rh
420	16	16.2	22	2	PQ0667	photosystem I 19.3
421	16	16.2	22	2	S67974	apolioprotein Cpl
422	16	16.2	22	2	A23441	tumor necrosis fac
423	16	16.2	22	2	B49732	NADH2 dehydrogenas
424	16	16.2	23	2	JP0062	ribosomal protein
425	16	16.2	23	2	B04348	internal peptide V
426	16	16.2	23	2	G64520	hypoethetical prote
427	16	16.2	23	2	T44539	hypoethetical prote
428	16	16.2	23	2	S37491	hypoethetical prote
429	16	16.2	23	2	A60226	pyruvate dehydroge
430	16	16.2	24	2	S23631	cytochrome-c oxida
431	16	16.2	24	2	A33262	heparin-binding gr
432	16	16.2	24	2	I45851	adenosylmethionine
433	16	16.2	24	2	PH1909	T-cell receptor al
434	16	16.2	24	2	SS1064	ribosomal protein
435	16	16.2	24	2	B56978	collagen alpha 2(X
436	16	16.2	24	2	A05298	fibrinogen gamma c
437	16	16.2	24	2	S10681	probable 7-ethoxyc
438	16	16.2	24	2	S35641	DNA (cytosine-5')-
439	16	16.2	24	2	F45357	Kex2/subtilisin-11
440	16	16.2	24	2	C45357	Kex2/subtilisin-11
441	16	16.2	24	2	A84023	hypoethetical prote
442	16	16.2	25	2	S22221	peroxidase (EC 1.1
443	16	16.2	25	2	JH0701	omega-conotoxin MV
444	16	16.2	25	2	F49533	T-cell receptor be
445	16	16.2	25	2	S58385	T-cell receptor al
446	16	16.2	25	2	S26233	ribosomal protein
447	16	16.2	25	2	T06233	ribosomal protein
448	16	16.2	25	2	I38002	calcium channel be
449	16	16.2	25	2	S00329	beta-N-acetylgluco
450	16	16.2	25	2	A60286	heat-stable serine
451	16	16.2	25	2	T09588	MADS box protein P
452	16	16.2	25	2	C25629	cytochrome-c oxida
453	16	16.2	25	2	S71387	alpha-2-macroglobu
454	16	16.2	25	2	S22234	vitronectin - chic
455	16	16.2	25	2	B86074	hypoethetical prote
456	16	16.2	25	2	A56864	membrane alanyl am
457	15.5	15.7	14	2	PA0045	porin por1 - Arabi
458	15.5	15.7	18	2	A35704	cytochrome P450 ol
459	15.5	15.7	12	2	S78007	fucosyltransferase
460	15.5	15.7	22	2	S55236	T669 kinase - huma
461	15.5	15.7	23	2	I50174	collagen alpha 1(I
462	15.5	15.7	24	2	PH1696	Ig heavy chain V r
463	15	15.2	3	4	GKHU	growth-modulating
464	15	15.2	7	2	A35039	hypoethetical colla
465	15	15.2	7	2	A44428	platelet aggregati
466	15	15.2	7	2	PT0579	T-cell receptor mo
467	15	15.2	7	2	A38671	peptidylglycine de
468	15	15.2	8	2	A21440	variant surface g1
469	15	15.2	8	2	I48934	apolipoprotein A-I
470	15	15.2	8	2	PT0691	T-cell receptor be
471	15	15.2	9	2	PT0288	Ig heavy chain CRD
472	15	15.2	9	2	A37027	macrophage chemota
473	15	15.2	9	2	C60070	gastrin - domestic
474	15	15.2	10	2	S09387	Pv1 protein - huma
475	15	15.2	10	2	S70721	heat shock protein
476	15	15.2	10	2	S43631	cytochrome-c oxida
477	15	15.2	10	2	S77990	cytochrome-c oxida
478	15	15.2	10	2	PT0289	Ig heavy chain CRD
479	15	15.2	10	2	PH0894	T-cell receptor be
480	15	15.2	11	2	D61033	ranacthykinin D -
481	15	15.2	11	2	S45386	low density lipopr
482	15	15.2	12	1	JTG50	tremerogen A-10 -
483	15	15.2	12	2	C36201	1-aminocyclopropan
484	15	15.2	12	2	PH1675	Ig heavy chain V r
485	15	15.2	12	2	A39233	myosin heavy chain
486	15	15.2	12	2	A44874	proboscipedia - fir
487	15	15.2	12	2	G49215	urease (EC 3.5.1.5
488	15	15.2	12	2	S49547	hypoethetical prote
489	15	15.2	12	2	A35585	cytokinin-binding
490	15	15.2	12	2	A55837	5-aminimidazole r
491	15	15.2	12	2	S43170	kinesin light chal
492	15	15.2	12	2	PH1180	T-cell receptor al
493	15	15.2	12	2	PH0802	T-cell receptor al
494	15	15.2	12	2	PH0790	T-cell receptor al
495	15	15.2	12	4	PC2123	amino transferase c
496	15	15.2	13	2	PH1676	Ig heavy chain V r
497	15	15.2	13	2	S46210	collagen alpha 1(V
498	15	15.2	13	2	PC1008	40K extracellular
499	15	15.2	13	2	S28425	20K protein - rape
500	15	15.2	13	2	S47390	T-cell antigen rec
501	15	15.2	13	2	PH0788	T-cell receptor al
502	15	15.2	14	1	BSRD	bombesin - fire-be
503	15	15.2	14	1	LFECW	trp operon leader
504	15	15.2	14	1	LFEBWC	trp operon leader
505	15	15.2	14	1	LFEBWT	trp operon leader
506	15	15.2	14	2	PH1677	Ig heavy chain V r
507	15	15.2	14	2	E90858	trp operon leader
508	15	15.2	14	2	S74128	superoxide dismuta
509	15	15.2	14	2	PQ0152	18K iron-sulfur pr
510	15	15.2	14	2	PT0294	Ig heavy chain CRD
511	15	15.2	14	2	PH1348	Ig heavy chain DJ
512	15	15.2	14	2	PH1356	Ig heavy chain DJ
513	15	15.2	14	2	PH1597	Ig H chain V-D-J r
514	15	15.2	14	2	PH0792	T-cell receptor al
515	15	15.2	14	2	A23996	beta-granulin - rat
516	15	15.2	14	2	PH0915	T-cell receptor be
517	15	15.2	14	2	B85761	trp operon leader
518	15	15.2	15	2	S26524	T-cell receptor al
519	15	15.2	15	2	S36888	ribosomal protein
520	15	15.2	15	2	PQ0017	terminal protein -
521	15	15.2	15	2	A60929	dichloromethane de
522	15	15.2	15	2	B60929	dichloromethane de
523	15	15.2	15	2	S71920	protease ECP 32
524	15	15.2	15	2	PA0051	protein QF20016 -
525	15	15.2	15	2	A32971	heparin-binding le
526	15	15.2	15	2	PH1365	Ig heavy chain DJ
527	15	15.2	15	2	S05700	insulin-like growt
528	15	15.2	15	2	S57577	T cell receptor V-
529	15	15.2	15	2	PN0665	dystrrophin-associa
530	15	15.2	15	2	F44833	synaptosomal-assoc
531	15	15.2	15	2	PD0444	coupling factor 6
532	15	15.2	15	2	I78838	fl3 ligand isofor
533	15	15.2	15	2	PH0751	T-cell receptor be
534	15	15.2	15	2	G35141	T-cell receptor de
535	15	15.2	15	2	PA0041	plastoquinol-Plast
536	15	15.2	15	4	I38032	hypoethetical MN1/T
537	15	15.2	15	4	I38031	hypoethetical MN1/T
538	15	15.2	16	2	G29501	fibrinopeptide A -
539	15	15.2	16	2	S05703	homeotic protein C
540	15	15.2	16	2	D58501	26K kidney and gal

541	15	15.2	16	2	S09700	phycobilliprotein 1	614	15	15.2	20	2	B53592	H+-exporting ATPase
542	15	15.2	16	2	B60278	24k antigen - Myco	615	15	15.2	21	2	A41154	ethylene-forming e
543	15	15.2	16	2	B44896	heat shock protein	616	15	15.2	21	2	S68023	nucleoside-diphosp
544	15	15.2	16	2	G24304	ribosomal protein	617	15	15.2	21	2	A27719	trypsin (EC 3.4.21
545	15	15.2	16	2	A41170	photosystem II 6.1	618	15	15.2	21	2	A61413	interferon alpha (
546	15	15.2	16	2	PA0103	L-lactate dehydrog	619	15	15.2	21	2	PH1688	Ig heavy chain V r
547	15	15.2	16	2	CA9048	T-cell receptor be	620	15	15.2	21	2	S02643	RNA-directed RNA p
548	15	15.2	16	2	A49255	T-cell receptor be	621	15	15.2	21	2	JH0361	casein - goldfist
549	15	15.2	16	2	PH1638	Ig H chain V-D-J r	622	15	15.2	21	2	JU0386	nitrile hydratase
550	15	15.2	16	2	D49037	TCR delta chain V-	623	15	15.2	21	2	A59325	probable bacteriop
551	15	15.2	16	2	A61530	tri-ose-phosphate i	624	15	15.2	21	2	S78416	ribosomal protein
552	15	15.2	16	2	D83865	hypothetical prote	625	15	15.2	21	2	A59429	dart gland peptide
553	15	15.2	16	4	A33171	hypothetical prote	626	15	15.2	22	2	C46285	formaldehyde dehyd
554	15	15.2	17	2	C37520	glutathione transf	627	15	15.2	22	2	S58433	isocitrate dehydro
555	15	15.2	17	2	B20242	pyruvate kinase (E	628	15	15.2	22	2	PH1325	interferon alpha (
556	15	15.2	17	2	B61334	trypsin (EC 3.4.21	629	15	15.2	22	2	PH1678	Ig heavy chain V r
557	15	15.2	17	2	S26744	Ig heavy chain J r	630	15	15.2	22	2	PH1679	Ig heavy chain V r
558	15	15.2	17	2	PH1754	T-cell receptor al	631	15	15.2	22	2	PH1721	Ig heavy chain V r
559	15	15.2	17	2	JP0046	ribosomal protein	632	15	15.2	22	2	PH1680	ribosomal protein
560	15	15.2	17	2	A34835	ribosomal protein	633	15	15.2	22	2	JP0071	collagen alpha 1(I
561	15	15.2	17	2	A34835	ryanodine receptor	634	15	15.2	22	2	D56978	GTP-binding, regula
562	15	15.2	17	2	I58087	unidentified prote	635	15	15.2	22	2	I45904	hypothetical prote
563	15	15.2	17	2	A61518	bombolitin IV - Am	636	15	15.2	22	2	S73389	T-cell receptor be
564	15	15.2	17	2	A60570	Ig mu heavy chain	637	15	15.2	22	2	PH1912	T-cell receptor J-
565	15	15.2	17	2	S57556	T-cell receptor be	638	15	15.2	22	2	S47209	albumin - rat (fra
566	15	15.2	17	2	PH0757	ribosomal protein	639	15	15.2	22	2	I51830	folate binding pro
567	15	15.2	17	2	S78421	Ig heavy chain DJ	640	15	15.2	22	2	S62670	hypothetical prote
568	15	15.2	18	2	PH1368	photosystem I prot	641	15	15.2	22	2	H83991	NADH2 dehydrogenas
569	15	15.2	18	2	A24749	neuropeptide A - b	642	15	15.2	22	2	H49732	cytochrome-c oxida
570	15	15.2	18	2	I52623	Ig heavy chain DJ	643	15	15.2	22	2	S43632	paralytic peptide
571	15	15.2	18	2	PH1349	T-cell receptor be	644	15	15.2	23	2	B39855	cryptidin - mouse (
572	15	15.2	18	2	PH0768	T-cell receptor be	645	15	15.2	23	2	I48936	cryptidin - western
573	15	15.2	18	2	B48839	TCR delta chain V-	646	15	15.2	23	2	I49413	T-cell receptor J-
574	15	15.2	18	2	G49037	Ig heavy chain DJ	647	15	15.2	23	2	S47192	Ig heavy chain DJ
575	15	15.2	19	2	PH1304	Ig heavy chain DJ	648	15	15.2	23	2	PH1361	Ig heavy chain DJ
576	15	15.2	19	2	PH1307	gamma crystallin I	649	15	15.2	23	2	PH1364	Ig heavy chain V r
577	15	15.2	19	2	A60894	beta-galactoside-b	650	15	15.2	23	2	PH1681	Ig heavy chain V r
578	15	15.2	19	2	PX0062	nitrogen fixation	651	15	15.2	23	2	PH1682	Ig heavy chain V r
579	15	15.2	19	2	S32675	ribosomal protein	652	15	15.2	23	2	PH1689	Ig heavy chain V r
580	15	15.2	19	2	JP0054	S-locus specific g	653	15	15.2	23	2	PH1693	Ig heavy chain V r
581	15	15.2	19	2	E56661	small granule S2 c	654	15	15.2	23	2	PH1694	Ig heavy chain V r
582	15	15.2	19	2	PC1309	transhyretin - bu	655	15	15.2	23	2	PH1695	Ig heavy chain V r
583	15	15.2	19	2	A49192	Ig heavy chain DJ	656	15	15.2	23	2	I33084	ribosomal protein
584	15	15.2	19	2	PH1360	phospholipase A2 (	657	15	15.2	23	2	A61574	leukocyte glycopro
585	15	15.2	19	2	PS0332	hypothetical prote	658	15	15.2	23	2	B26091	cystic fibrosis tr
586	15	15.2	19	2	S25715	Qa-2 antigen - mou	659	15	15.2	23	2	I51922	internal peptide V
587	15	15.2	19	2	S12268	TCR delta chain V-	660	15	15.2	23	2	A04348	4-hydroxyphenylpyr
588	15	15.2	19	2	I49037	enhancing factor -	661	15	15.2	23	2	S74178	hypothetical prote
589	15	15.2	19	2	S29495	urease (EC 3.5.1.5	662	15	15.2	23	2	S32727	Ig heavy chain DJ
590	15	15.2	20	2	H49215	15K protein B - ra	663	15	15.2	23	2	PH1303	tyrosine kinase su
591	15	15.2	20	2	B38382	Ig heavy chain CDR	664	15	15.2	23	2	A56357	brain-type creatin
592	15	15.2	20	2	JP0070	ribosomal protein	665	15	15.2	23	2	PC2199	alicyclic amine N-
593	15	15.2	20	2	JP0060	ribosomal protein	666	15	15.2	24	2	I53473	phosphoprotein pho
594	15	15.2	20	2	JP0059	gamma crystallin V	667	15	15.2	24	2	PH0084	fatty acid-binding
596	15	15.2	20	2	D60894	ribulose-bisphosph	668	15	15.2	24	2	B60422	MSEL-neurophysin -
597	15	15.2	20	2	S07232	lens fiber cell me	669	15	15.2	24	2	S42785	relaxin - baboon (
598	15	15.2	20	2	E34490	lens fiber cell me	670	15	15.2	24	2	PT0256	Ig heavy chain CDR
599	15	15.2	20	2	C34490	Dnak protein homol	671	15	15.2	24	2	PH1683	Ig heavy chain V r
600	15	15.2	20	2	PC4384	jacalin beta-I cha	672	15	15.2	24	2	PH1684	Ig heavy chain V r
601	15	15.2	20	2	S29636	glutamyl-tRNA redu	673	15	15.2	24	2	PH1685	Ig heavy chain V r
602	15	15.2	20	2	S48702	glutathione S-trans	674	15	15.2	24	2	PH1686	Ig heavy chain V r
603	15	15.2	20	2	PC1152	glutathione S-trans	675	15	15.2	24	2	PH1687	Ig heavy chain V r
604	15	15.2	20	2	S19618	glutathione S-trans	676	15	15.2	24	2	PH1688	Ig heavy chain V r
605	15	15.2	20	2	S28405	lamin B receptor -	677	15	15.2	24	2	PH1689	Ig heavy chain V r
606	15	15.2	20	2	S28405	Ig heavy chain DJ	678	15	15.2	24	2	PH1690	Ig heavy chain V r
607	15	15.2	20	2	PH1341	Ig heavy chain DJ	679	15	15.2	24	2	PH1691	Ig heavy chain V r
608	15	15.2	20	2	PH1338	neurofilament heav	680	15	15.2	24	2	PH1692	Ig heavy chain V r
609	15	15.2	20	2	I53671	T cell receptor al	681	15	15.2	24	2	PH1693	Ig heavy chain V r
610	15	15.2	20	2	PH1783	82k protein - bovi	682	15	15.2	24	2	PH1694	Ig heavy chain V r
611	15	15.2	20	2	S31220	ribosomal protein	683	15	15.2	24	2	A61141	T-cell receptor be
612	15	15.2	20	2	S78763	ribosomal protein	684	15	15.2	24	2	A61505	callectulin, panc
613	15	15.2	20	2	S78763	ribosomal protein	685	15	15.2	24	2	S02073	pollen allergen Ph
							686	15	15.2	24	2		photosystem II 10k

687	15	15.2	24	2	PC2312	X-pro aminopeptidase
688	15	15.2	24	2	PC2313	X-pro aminopeptidase
689	15	15.2	24	2	S37383	rRNA N-glycosidase
690	15	15.2	24	2	T24611	hypothetical prote
691	15	15.2	24	2	154329	gene NF1 protein -
692	15	15.2	24	2	D85955	hypothetical prote
693	15	15.2	24	2	G85602	hypothetical prote
694	15	15.2	25	1	JC4278	ribosomal protein
695	15	15.2	25	1	PH1686	Ig heavy chain V r
696	15	15.2	25	2	PH1700	Ig heavy chain V r
697	15	15.2	25	2	PH1701	Ig heavy chain V r
698	15	15.2	25	2	S07770	histone H2B.1, spe
699	15	15.2	25	2	S49025	ribosomal protein
700	15	15.2	25	2	JP0044	ribosomal protein
701	15	15.2	25	2	JQ1617	ribosomal protein
702	15	15.2	25	2	JC4685	ribosomal protein
703	15	15.2	25	2	S38425	ribosomal protein
704	15	15.2	25	2	T49214	ribosomal protein
705	15	15.2	25	2	I56978	collagen alpha 2(X
706	15	15.2	25	2	A60921	uroepithelial cell
707	15	15.2	25	2	I67422	gene GLO14 protein
708	15	15.2	25	2	S25434	gene CP1 leader p
709	15	15.2	25	2	S13996	hypothetical prote
710	15	15.2	25	2	S21515	flmp protein - Esc
711	15	15.2	25	2	JP0064	ribosomal protein
712	15	15.2	25	2	T01689	large granule r1 c
713	15	15.2	25	2	PC1314	HHA-DB1 exon2 pro
714	15	15.2	25	2	S44201	histidine-rich pro
715	15	15.2	18	2	B32473	acidolysin (EC 3.4
716	14.5	14.6	19	2	A60152	hull allergen gly
717	14.5	14.6	20	2	A57106	T-cell receptor al
718	14.5	14.6	22	2	S03459	flucosyltransferase
719	14.5	14.6	22	2	S48196	carbon-monoxide de
720	14	14.1	4	2	PL0140	CoI intron 16 prot
721	14	14.1	4	2	I38888	hypothetical prote
722	14	14.1	5	2	S53595	sarcosine dehydrog
723	14	14.1	6	2	A61419	jacalin beta-II ch
724	14	14.1	6	2	S29637	collagen alpha 1(I
725	14	14.1	6	2	B56979	gramicidin S synth
726	14	14.1	7	2	S42407	hypothetical prote
727	14	14.1	7	2	B33541	Ig mu chain D regl
728	14	14.1	7	2	E33932	glutathione S-tran
729	14	14.1	7	2	S66442	glutathione S-tran
730	14	14.1	7	2	S45648	Na+-transporting A
731	14	14.1	7	4	S15597	ort 4 rara 5'-regi
732	14	14.1	8	2	S20162	leghemoglobin III
733	14	14.1	8	2	I64832	Ca2+-transporting
734	14	14.1	9	2	S59902	glutathione transf
735	14	14.1	9	2	S07205	litorin 2-Glu - Au
736	14	14.1	9	2	S07204	litorin I - Austri
737	14	14.1	9	2	S07241	litorin - Robde's
738	14	14.1	9	2	CA1170	photosystem II pro
739	14	14.1	9	2	PT0285	Ig heavy chain CRD
740	14	14.1	9	2	S65913	pyrimidine synthe
741	14	14.1	9	2	PC7076	spectrin alpha cha
742	14	14.1	10	2	A61289	streptopain (EC 3.
743	14	14.1	10	2	PC0177	neuromedin C - lau
744	14	14.1	10	2	A60647	neuromedin C - bov
745	14	14.1	10	2	H60787	sperm-activating p
746	14	14.1	10	2	H60787	sperm-activating p
747	14	14.1	10	2	D60788	sperm-activating p
748	14	14.1	10	2	B60787	sperm-activating p
749	14	14.1	10	2	A60788	sperm-activating p
750	14	14.1	10	2	C60589	sperm-activating p
751	14	14.1	10	2	D60588	sperm-activating p
752	14	14.1	10	2	XGMB	ethinocyte membra
753	14	14.1	10	2	A46030	gonadoliberin I -
754	14	14.1	10	2	A21114	gonadoliberin - ch
755	14	14.1	10	2	A30823	bohrpoxstoxin - ja
756	14	14.1	10	2	I48778	small nuclear ribo
757	14	14.1	10	2	PT0632	T-cell receptor be
758	14	14.1	10	2	PT0664	T-cell receptor be
759	14	14.1	10	2	PT0215	T-cell receptor be
760	14	14.1	10	2	PX0060	lysosome-associate
761	14	14.1	10	2	A59173	nuclease BHL (EC 3
762	14	14.1	10	2	PA0116	ferridoxin-NADP re
763	14	14.1	10	2	PS0220	ferridoxin-NADP re
764	14	14.1	11	2	YHRT	morphogenetic neur
765	14	14.1	11	2	YHRT	morphogenetic neur
766	14	14.1	11	2	YHRT	morphogenetic neur
767	14	14.1	11	2	YHRT	morphogenetic neur
768	14	14.1	11	2	YHRT	morphogenetic neur
769	14	14.1	11	2	YHRT	morphogenetic neur
770	14	14.1	11	2	YHRT	morphogenetic neur
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783	14	14.1	11	2	YHRT	morphogenetic neur
784	14	14.1	11	2	YHRT	morphogenetic neur
785	14	14.1	11	2	YHRT	morphogenetic neur
786	14	14.1	11	2	YHRT	morphogenetic neur
787	14	14.1	11	2	YHRT	morphogenetic neur
788	14	14.1	11	2	YHRT	morphogenetic neur
789	14	14.1	11	2	YHRT	morphogenetic neur
790	14	14.1	11	2	YHRT	morphogenetic neur
791	14	14.1	11	2	YHRT	morphogenetic neur
792	14	14.1	11	2	YHRT	morphogenetic neur
793	14	14.1	11	2	YHRT	morphogenetic neur
794	14	14.1	11	2	YHRT	morphogenetic neur
795	14	14.1	11	2	YHRT	morphogenetic neur
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797	14	14.1	11	2	YHRT	morphogenetic neur
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799	14	14.1	11	2	YHRT	morphogenetic neur
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801	14	14.1	11	2	YHRT	morphogenetic neur
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803	14	14.1	11	2	YHRT	morphogenetic neur
804	14	14.1	11	2	YHRT	morphogenetic neur
805	14	14.1	11	2	YHRT	morphogenetic neur
806	14	14.1	11	2	YHRT	morphogenetic neur
807	14	14.1	11	2	YHRT	morphogenetic neur
808	14	14.1	11	2	YHRT	morphogenetic neur
809	14	14.1	11	2	YHRT	morphogenetic neur
810	14	14.1	11	2	YHRT	morphogenetic neur
811	14	14.1	11	2	YHRT	morphogenetic neur
812	14	14.1	11	2	YHRT	morphogenetic neur
813	14	14.1	11	2	YHRT	morphogenetic neur
814	14	14.1	11	2	YHRT	morphogenetic neur
815	14	14.1	11	2	YHRT	morphogenetic neur
816	14	14.1	11	2	YHRT	morphogenetic neur
817	14	14.1	11	2	YHRT	morphogenetic neur
818	14	14.1	11	2	YHRT	morphogenetic neur
819	14	14.1	11	2	YHRT	morphogenetic neur
820	14	14.1	11	2	YHRT	morphogenetic neur
821	14	14.1	11	2	YHRT	morphogenetic neur
822	14	14.1	11	2	YHRT	morphogenetic neur
823	14	14.1	11	2	YHRT	morphogenetic neur
824	14	14.1	11	2	YHRT	morphogenetic neur
825	14	14.1	11	2	YHRT	morphogenetic neur
826	14	14.1	11	2	YHRT	morphogenetic neur
827	14	14.1	11	2	YHRT	morphogenetic neur
828	14	14.1	11	2	YHRT	morphogenetic neur
829	14	14.1	11	2	YHRT	morphogenetic neur
830	14	14.1	11	2	YHRT	morphogenetic neur
831	14	14.1	11	2	YHRT	morphogenetic neur
832	14	14.1	11	2	YHRT	morphogenetic neur

833	14	14.1	15	2	PA0062	fumarate hydratase	906	14	14.1	19	2	B29501	fibrinopeptide A -
834	14	14.1	15	2	A36279	chemottractant pr	907	14	14.1	19	2	C29501	fibrinopeptide A -
835	14	14.1	15	2	A36527	juvenile-hormone e	908	14	14.1	19	2	B56513	vitronectin
836	14	14.1	15	2	S43634	cytochrome-c oxida	909	14	14.1	19	2	PA0010	seed storage prote
837	14	14.1	15	2	S57201	basic proteinase I	910	14	14.1	19	2	H61491	seed protein ws-24
838	14	14.1	15	2	PH1314	Ig heavy chain DJ	911	14	14.1	19	2	T50329	wd-repeat protein
839	14	14.1	15	2	S03955	acidic fibroblast	912	14	14.1	19	2	B60977	14-3-3 protein hom
840	14	14.1	15	2	PQ0073	T-cell receptor be	913	14	14.1	19	2	JX0124	tachyplesin I prec
841	14	14.1	15	2	PQ0074	T-cell receptor be	914	14	14.1	19	2	S60110	hypothetical prote
842	14	14.1	15	2	PQ0097	glutathione peroxi	915	14	14.1	19	2	I49039	T-cell receptor be
843	14	14.1	15	2	PH1616	Ig H chain V-D-J r	916	14	14.1	19	2	A44356	37k adherens junct
844	14	14.1	15	2	PH0780	T-cell receptor al	917	14	14.1	19	2	S22232	vitronectin - goat
845	14	14.1	15	2	PH0806	T-cell receptor al	918	14	14.1	19	2	S22233	vitronectin - shee
846	14	14.1	15	2	PH0797	T-cell receptor al	919	14	14.1	19	2	S43045	translational elonga
847	14	14.1	15	2	E49037	TCR delta chain V-	920	14	14.1	20	2	A60728	cytochrome p450 3A
848	14	14.1	15	2	S71306	heat shock protein	921	14	14.1	20	2	S17461	flavodoxin B - Azo
849	14	14.1	15	2	S71396	dihydropyrimidin	922	14	14.1	20	2	A54083	p190/210, fatty ac
850	14	14.1	15	2	S66443	NMD(P) transhydrog	923	14	14.1	20	2	S29100	glutathione transf
851	14	14.1	15	2	PQ0780	NMDH2 dehydrogenas	924	14	14.1	20	2	A14344	alanine transamina
852	14	14.1	16	2	S17217	ribulose-bisphosph	925	14	14.1	20	2	A60489	venombin A (EC 3.4
853	14	14.1	16	2	A28144	ribosomal protein	926	14	14.1	20	2	D49215	urease (EC 3.5.1.5
854	14	14.1	16	2	S02473	coat protein Vp1 -	927	14	14.1	20	2	S46488	peptidylprolyl iso
855	14	14.1	16	2	E58501	25k kidney and gal	928	14	14.1	20	2	PX0059	trypsin inhibitor
856	14	14.1	16	2	S51610	hypothetical prote	929	14	14.1	20	2	S50741	probable trypsin i
857	14	14.1	16	2	P50210	28k protein 4209 -	930	14	14.1	20	2	B60505	hemoglobin Al-2 be
858	14	14.1	16	2	S28213	glutathione transf	931	14	14.1	20	2	D37396	gamma-crystallin I
859	14	14.1	16	2	A35552	caldesmon - turkey	932	14	14.1	20	2	A39543	pollen allergen Fe
860	14	14.1	16	2	PT0234	Ig heavy chain CDK	933	14	14.1	20	2	A44927	collagen alpha 1(I
861	14	14.1	16	2	PH1351	Ig heavy chain DJ	934	14	14.1	20	2	S60668	major outer membra
862	14	14.1	16	2	PH1317	Ig heavy chain DJ	935	14	14.1	20	2	S65746	hypothetical prote
863	14	14.1	16	2	B48406	annexin VI homolog	936	14	14.1	20	2	T48881	hypothetical prote
864	14	14.1	16	2	PH1453	T-cell receptor al	937	14	14.1	20	2	B39089	leader peptide flm
865	14	14.1	16	2	S10678	aldenhyde dehydroge	938	14	14.1	20	2	S18582	hydrogenase (EC 1.
866	14	14.1	16	2	D89854	conserved hypotet	939	14	14.1	20	2	S61278	hypothetical prote
867	14	14.1	17	1	A05168	conanotokin G [wall	940	14	14.1	20	2	E61497	nikkomycin synthas
868	14	14.1	17	1	S24570	Ig heavy chain J r	941	14	14.1	20	2	S65605	seed protein ws-20
869	14	14.1	17	2	B49404	T-cell receptor be	942	14	14.1	20	2	B60365	dimeric protein (B
870	14	14.1	17	2	B44873	caldesmon - rabbit	943	14	14.1	20	2	S77983	chymotrypsin inhib
871	14	14.1	17	2	A44560	terephthalate 1,2-	944	14	14.1	20	2	A34859	cytochrome-c oxida
872	14	14.1	17	2	S05033	photosystem II pro	945	14	14.1	20	2	PH1326	heliothermine - Mex
873	14	14.1	17	2	A27636	cyto toxin B - CloS	946	14	14.1	20	2	D49255	Ig heavy chain DJ
874	14	14.1	17	2	C37396	pollen allergen Fe	947	14	14.1	20	2	A49712	T-cell receptor be
875	14	14.1	17	2	A39111	Ig light chain - P	948	14	14.1	20	2	S03954	acidic fibroblast
876	14	14.1	17	2	PH1367	Ig heavy chain DJ	949	14	14.1	20	2	I46652	T-cell receptor de
877	14	14.1	17	2	I42755	interferon alpha (	950	14	14.1	20	2	A38689	I-phosphatidylinos
878	14	14.1	17	2	B49255	T-cell receptor be	951	14	14.1	20	2	A42267	J-kappa recombinat
879	14	14.1	17	2	B31769	T-cell receptor de	952	14	14.1	20	2	PX0061	beta-N-acetylgluco
880	14	14.1	17	2	E23734	insulin-like growt	953	14	14.1	20	2	A13050	pyruvate kinase (E
881	14	14.1	17	2	PH0794	T-cell receptor al	954	14	14.1	20	2	I58192	glial fibrillary a
882	14	14.1	17	2	A61019	17k basolateral pl	955	14	14.1	20	2	S66222	defensin AMP2 - Da
883	14	14.1	18	2	F49215	urease (EC 3.5.1.5	956	14	14.1	20	2	A85645	Amino terminal of
884	14	14.1	18	2	B49215	urease (EC 3.5.1.5	957	14	14.1	20	2	A58903	metalloproteinase
885	14	14.1	18	2	C40433	Nbda protein - Cya	958	14	14.1	20	2	D22565	R-phycoerythrin be
886	14	14.1	18	2	S03528	Ig heavy chain J1	959	14	14.1	21	2	PC2214	alanine-tRNA ligas
887	14	14.1	18	2	I52614	u-plasminogen acti	960	14	14.1	21	2	S16073	T-cell receptor J-
888	14	14.1	18	2	I51427	hemoglobin alpha c	961	14	14.1	21	2	PH1730	Ig heavy chain V r
889	14	14.1	18	2	C30309	histone H4 - Euplo	962	14	14.1	21	2	A60420	Iens Intrinsic mem
890	14	14.1	18	2	S46241	NMD(P)-H-flavin oxi	963	14	14.1	21	2	B60119	opacity protein P.
891	14	14.1	18	2	PN0175	glutathione transt	964	14	14.1	21	2	I40157	tetracycline resis
892	14	14.1	18	2	S70340	napin large chain	965	14	14.1	21	2	PC7043	rev protein - huma
893	14	14.1	18	2	S65454	aspergillopepsin I	966	14	14.1	21	2	PH1369	hypothetical prote
894	14	14.1	18	2	S63487	fibrinogenolytic p	967	14	14.1	21	2	S35676	ubiquitin carboxyl
895	14	14.1	18	2	PT0239	Ig heavy chain CDR	968	14	14.1	21	2	D48518	Ig heavy chain DJ
896	14	14.1	18	2	PH1350	Ig heavy chain DJ	969	14	14.1	21	2	F64121	protein kinase - r
897	14	14.1	18	2	S26664	microtubule-associ	970	14	14.1	21	2	S68971	PEB1 5'-region hyp
898	14	14.1	18	2	S71592	serine proteinase	971	14	14.1	21	2	PC7043	hypothetical prote
899	14	14.1	18	2	PH1815	T cell receptor al	972	14	14.1	21	2	S35676	ubiquitin carboxyl
900	14	14.1	18	2	C32537	T-cell receptor al	973	14	14.1	22	2	S58432	I protein kinase - r
901	14	14.1	18	2	I46653	T-cell receptor de	974	14	14.1	22	2	S05057	isocitrate dehydro
902	14	14.1	18	2	PL0025	T-cell surface gly	975	14	14.1	22	2	PT0431	3-methyl-2-oxobuta
903	14	14.1	18	2	S36120	lectin - Euphorbia	976	14	14.1	22	2	A36399	leucyl aminopeptid
904	14	14.1	19	2	PS0236	trypsin inhibitor	977	14	14.1	22	2	A35418	C-type natriuretic
905	14	14.1	19	2	S13046	calreticulin - rab	978	14	14.1	22	2		brain natriuretic

979	14	14.1	22	2	Jf0581	natuerine peptid
980	14	14.1	22	2	I41289	T-cell receptor be
981	14	14.1	22	2	S07966	T-cell receptor be
982	14	14.1	22	2	D32537	T-cell receptor al
983	14	14.1	22	2	S07701	T-cell receptor al
984	14	14.1	22	2	S47206	T-cell receptor J-I
985	14	14.1	22	2	H30608	Ig kappa chain V-I
986	14	14.1	22	2	B32711	leghemoglobin - LO
987	14	14.1	22	2	S68616	histone H1 - sea u
988	14	14.1	22	2	C64330	ribosomal protein
989	14	14.1	22	2	PM0048	estrogen receptor
990	14	14.1	22	2	S45058	coat protein - tur
991	14	14.1	22	2	S64675	collagen alpha 3(I
992	14	14.1	22	2	PO0143	polygalacturonase
993	14	14.1	22	2	PO0657	hemagglutinin [imp
994	14	14.1	22	2	T25653	hypothetical prote
995	14	14.1	22	2	S65370	tRNA-guanine trans
996	14	14.1	22	2	F84018	hypothetical prote
997	14	14.1	22	2	PC7072	H+-transporting tw
998	14	14.1	23	2	S51188	aldehyde dehydroge
999	14	14.1	23	2	A33105	dihydrofolate redu
1000	14	14.1	23	2	S65379	cytochrome-c oxida

## ALIGNMENTS

RESULT 1  
S48654  
Plasmeprin II - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 15-Jul-1995 #sequence\_revision 19-Apr-1996 #text\_change 09-Jun-2000  
C:Accession: S48654  
R:Hill, J.; Tyas, L.; Phylip, L.H.; Kay, J.; Dunn, B.M.; Berry, C.  
FEBS Lett. 352, 155-158, 1994  
A:Title: High level expression and characterisation of Plasmeprin II, an aspartic protease  
A:Reference number: S48654; MUID:95010698; PMID:7925966  
A:Accession: S48654  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-20 <HIL>

Query Match	30.3%	Score 30;	DB 2;	Length 20;
Best Local Similarity	45.5%	Pred. No. 1.9e+02;		
Matches	5;	Conservative	4;	Mismatches 2;
				Indels 0;
				Gaps 0;
1	NVPGHERMGRG	11		
3	SMTGQOMGRG	13		

RESULT 2  
E39855  
paralytic peptide III - beet armyworm  
C:Species: Spodoptera exigu (beet armyworm)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993  
C:Accession: E39855  
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.  
J. Biol. Chem. 266, 12873-12877, 1991  
A:Title: Isolation and identification of paralytic peptides from hemolymph of the lepidopteran pest, the beet armyworm, *Spodoptera exigu* (Lepidoptera: Noctuidae)  
A:Reference number: A39855; MUID:91302298; PMID:2071576  
A:Accession: E39855  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-23 <SKIT>  
A:Superfamily: paralytic peptide I

Query Match	30.3%	Score 30;	DB 2;	Length 23;
Best Local Similarity	50.0%	Pred. No. 2.2e+02;		
Matches	5;	Conservative	2;	Mismatches 3;
				Indels 0;
				Gaps 0;
QY	3	PGHEMGRGR	12	

Db 9 PGYQRTADGR 18

RESULT 3  
C39855  
paralytic peptide I - beet armyworm  
C:Species: Spodoptera exiguua (beet armyworm)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993  
C:Accession: C39855  
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.  
J. Biol. Chem. 266, 12873-12877, 1991  
A:Title: Isolation and identification of paralytic peptides from hemolymph of the lep  
A:Reference number: A39855; MUID:91302298; PMID:2071576  
A:Accession: C39855  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-23 <SKT>  
C:Superfamily: paralytic peptide I

Query Match	30.3%	Score 30:	DB 2:	Length 23:
Best Local Similarity	50.0%	Pred. No.	2.2e+02:	
Matches	5:	Conservative	2:	Mismatches 3:
				Indels 0:
				Gaps 0:

QY	3	PCHERMGRGR	12
		::	
Db	9	PGYQRTADGR	18

RESULT 4  
D39855  
paralytic peptide II - beet armyworm  
C:Species: Spodoptera exigu(a) (beet armyworm)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993  
C:Accession: D39855  
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.  
J. Biol. Chem. 266, 12873-12877, 1991  
A:Title: Isolation and identification of paralytic peptides from hemolymph of the lep  
A:Reference number: A39855; MUID:91302298; PMID:2071576  
A:Accession: D39855  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-23 <SKI>  
A:Superfamily: paralytic peptide I

Query	March	Score	30	DB	2	Length	23
Best Local Similarity	50.0%	Pred.	No.	2	2e+02		
Matches	5	Conservative	2	Mismatches	3	Indels	0
						Gaps	0
OY	3	PGHERMGNGR	12				
		::					
Db	9	PGYQRTADGR	18				

RESULT 5  
155453  
zinc finger homeodomain protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 15-Oct-1999  
C:Accession: 155453  
R:Mura, Y.; Tam, T.; Ido, A.; Morinaga, T.; Miki, T.; Hashimoto, T.; Tamaoki, T.  
J. Biol. Chem. 270, 26840-26848, 1995  
A:Title: Cloning and characterization of an ATG1 isoform that expresses in a neurona  
A:Reference number: 155453; MUID:96070776; PMID:7552926  
A:Accession: 155453  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-18 <RES>  
A:Cross-references: GB:I32833, NID:g976348, PIDN:AMC37582.1, PID:g976349  
A:Superfamily: alpha-fetoprotein enhancer-binding protein; homeobox homology  
A:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match	29.3%;	Score 29;	DB 2;	Length 18;
Best Local Similarity	50.0%;	Pred. No.	2.5e+02;	

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 RMGRGRSTSKEL 18  
1:1 1:1 1:1

Db 2 RLGGSQVSEEL 13

RESULT 6  
F39855  
paralytic peptide I - tobacco budworm

C:Species: Heliothis virescens (tobacco budworm)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993

C:Accession: F39855  
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.

J. Biol. Chem. 266, 12873-12877, 1991

A:Title: Isolation and identification of paralytic peptides from hemolymph of the lepidopteran tobacco budworm

A:Reference number: A39855; MUID:91302298; PMID:2071576

A:Accession: F39855  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-23 <SKI>

Superfamily: paralytic peptide I

Query Match 29.3%; Score 29; DB 2; Length 23;

Best Local Similarity 45.5%; Pred. No. 3.2e+02;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VPGHERMGRGR 12  
1:1 1:1 1:1

Db 8 IPGYMRTADGR 18

RESULT 7

G39855  
paralytic peptide II - tobacco budworm

C:Species: Heliothis virescens (tobacco budworm)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993

C:Accession: G39855  
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.

J. Biol. Chem. 266, 12873-12877, 1991

A:Title: Isolation and identification of paralytic peptides from hemolymph of the lepidopteran tobacco budworm

A:Reference number: A39855; MUID:91302298; PMID:2071576

A:Accession: G39855  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-23 <SKI>

Superfamily: paralytic peptide I

Query Match 29.3%; Score 29; DB 2; Length 23;

Best Local Similarity 45.5%; Pred. No. 3.2e+02;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VPGHERMGRGR 12  
1:1 1:1 1:1

Db 8 IPGYMRTADGR 18

RESULT 8

A31963  
pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain type I - pig roundworm (frag)

C:Species: Ascaris suum (pig roundworm)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 12-Sep-1997

C:Accession: A31963  
R:Thissen, J.; Komuniecki, R.

J. Biol. Chem. 263, 19092-19097, 1988

A:Title: Phosphorylation and inactivation of the pyruvate dehydrogenase from the anaerobic roundworm

A:Reference number: A31963; MUID:89066711; PMID:3198613

A:Accession: A31963  
A:Status: preliminary  
A:Molecule type: protein

A:Residues: 1-16 <THI>  
C:Keywords: mitochondrion; oxidoreductase; phosphoprotein

Query Match 25.3%; Score 25; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 1e+03;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GHERMGRSTSS 15  
1:1 1:1 1:1

Db 3 GHSSMDPTSS 14

RESULT 9

PL0143  
carbon monoxide dehydrogenase (EC 1.2.99.2) medium chain - Pseudomonas carboxydohydro

C:Species: Pseudomonas carboxydohydrog

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 28-Apr-1993

C:Accession: PL0143  
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.

Arch. Microbiol. 152, 335-341, 1989

A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydot

A:Reference number: PL0138; MUID:90055678; PMID:2818128

A:Accession: PL0143  
A:Molecule type: protein  
A:Residues: 1-15 <KRA>  
C:Comment: Carbon monoxide dehydrogenase consists of three polypeptide chains: large,

Query Match 24.2%; Score 24; DB 2; Length 15;

Best Local Similarity 75.0%; Pred. No. 1.4e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPGH 5  
1:1 1:1 1:1

Db 3 IPGH 6

RESULT 10

PH0766  
T-cell receptor beta chain (J3) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999

C:Accession: PH0766  
R:Caanover, J.L.; Romero, P.; Wilmann, C.; Koulitsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0766  
A:Molecule type: mRNA

A:Residues: 1-16 <CAS>  
A:Cross-references: EMBL:X60860; NID:952745; PIDN:CMA43250.1; PID:952746

A:Experimental source: T lymphocyte  
C:Keywords: T-cell receptor

Query Match 24.2%; Score 24; DB 2; Length 16;

Best Local Similarity 57.1%; Pred. No. 1.5e+03;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 KGRITSSK 16  
1:1 1:1 1:1

Db 6 KGRITNER 12

RESULT 11

C30221  
histone H2A 8 - chicken (fragment)

C:Species: Gallus gallus (chicken)  
C:Date: 02-Nov-1989 #sequence\_revision 02-Nov-1989 #text\_change 30-Sep-1993

C:Accession: C30221  
R:Challoner, P.B.; Moss, S.B.; Groudine, M.

Mol. Cell. Biol. 9, 902-913, 1989

A:Title: Expression of replication-dependent histone genes in avian spermatids involve

A:Reference number: A30221; MUID:89261754; PMID:2471062

A:Accession: C30221  
A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA  
A:Residues: 1-17 <CH>

Query Match 24.2%; Score 24; DB 2; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.6e+03;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 9 GRGRSSKELA 19  
|||: |  
Db 3 GRGKGCKARA 13

## RESULT 12

B24735  
glutathione transferase (EC 2.5.1.18) 1-2 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)  
C>Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 18-Jun-1993

C:Accession: B24735

R:Mannevik, B.; Allin, P.; Gutheberg, C.; Jenson, H.; Tahlir, M.K.; Warholm, M.; Jorvæ

Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985

A:Title: Identification of three classes of cytosolic glutathione transferase common to

A:Reference number: A24735; MUID:86042634; PMID:3864155

A:Accession: B24735

A:Molecule type: protein

C:Superfamily: glutathione transferase

C:Keywords: transferase

Query Match 24.2%; Score 24; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 7; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

OY 3 PG----HERMGRGR 12  
|||: |  
Db 1 PGKPVLRHFRNGR 14

## RESULT 13

S28396

T-complex protein 1 - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 04-Sep-1998

C:Accession: S28396

R:Frydman, J.; Nimmegern, E.; Erdjument-Bromage, H.; Wall, J.S.; Tempst, P.; Hartl, F.U

EMBO J. 11, 4767-4778, 1992

A:Title: Function in protein folding of TRIC, a cytosolic ring complex containing TCP-1

A:Reference number: S28395; MUID:93099850; PMID:1361170

A:Accession: S28396

A:Molecule type: protein

C:Superfamily: molecular chaperone t-complex-type

Query Match 24.2%; Score 24; DB 2; Length 19;  
Best Local Similarity 42.9%; Pred. No. 1.8e+03;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 6 ERMGGRSTSKELA 19  
:|:|:|:|  
Db 4 DEVGDTTSVTYLA 17

## RESULT 14

S29858

ribosomal protein S7 - Thermococcus celer (fragment)

C:Species: Thermococcus celer

C>Date: 08-Dec-1993 #sequence\_revision 01-Dec-1995 #text\_change 17-Mar-1999

C:Accession: S29858

R:Klenk, H.P.; Schwass, V.; Zillig, W.

Biochim. Biophys. Acta 1172, 236-238, 1993

A:Title: Nucleotide sequence of the genes encoding proline tRNA(UGC) and threonine tRNA(C

A:Reference number: S29858; MUID:93176822; PMID:7916630

A:Accession: S29858

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: nucleic acid

A:Residues: 1-21 <KLE>

A:Cross-references: EMBL:X68397

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

Query Match 24.2%; Score 24; DB 2; Length 21;  
Best Local Similarity 42.9%; Pred. No. 2e+03;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 6 ERMGGRSTSKELA 19  
:|:|:|:|  
Db 7 QOGRDRSDPYLA 20

## RESULT 15

I50535

calmodulin - electric eel (fragment)

C:Species: Electrophorus electricus (electric eel)

C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C:Accession: I50535

R:Munjaal, R.P.; Chandra, T.; WOO, S.L.C.; Dedman, J.R.; Means, A.R.

Proc. Natl. Acad. Sci. U.S.A. 78, 2330-2334, 1981

A:Title: A cloned calmodulin structural gene probe is complementary to DNA sequences

A:Reference number: I50535; MUID:81223873; PMID:6941292

A:Accession: I50535

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-21 <MUN>

A:Cross-references: GB:M17495; NID:9213132; PIDN:AAA49237.1; PID:9213133

Query Match 24.2%; Score 24; DB 2; Length 21;  
Best Local Similarity 38.5%; Pred. No. 2e+03;  
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 6 ERMGGRSTSKEL 18  
:|:|:|:|  
Db 1 DKEGNGYISAEEL 13

## RESULT 16

PC4030

rRNA endonuclease (EC 3.1.27.10) - shiitake mushroom (fragment)

N:Alternate names: nuclease Ie3

C:Species: Lentinula edodes (shiitake mushroom)

C>Date: 21-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 20-Mar-1996

C:Accession: PC4030

R:Kobayashi, H.; Inokuchi, N.; Koyama, T.; Tomita, M.; Irie, M.

Biosci. Biotechnol. Biochem. 59, 1169-1171, 1995

A:Title: Purification and characterization of the 2nd 5'-nucleotide-forming nuclease

A:Reference number: PC4030; MUID:95337563; PMID:7613009

A:Accession: PC4030

A:Molecule type: DNA

A:Residues: 1-23 <ROB>

C:Comment: This enzyme has 3'-nucleotidase activity.

C:Keywords: endonuclease; hydrolase

Query Match 24.2%; Score 24; DB 2; Length 23;  
Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 GHERMG 9  
||:|:|  
Db 5 GHLEVG 10

## RESULT 17

S40666

hypothetical protein 2 - wheat dwarf virus

C:Species: wheat dwarf virus

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 17-Mar-1999

C:Accession: S40666

R:Decker, E.L.; Woolston, C.J.; Xue, Y.; Cox, B.; Mullineaux, P.M.

Nucleic Acids Res. 19, 4075-4081, 1991



A:Title: Transcript mapping reveals different expression strategies for the bicistronic  
A:Reference number: S40665; MUID:9133411; PMID:1870964  
A:Accession: S40666  
A>Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-24 <DEK>

Query Match 24.2%; Score 24; DB 2; Length 24;  
Best Local Similarity 75.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPGH 5  
DB 15 IPGH 18

RESULT 18  
S78415  
ribosomal protein Rl27, mitochondrial [validated] - rat (tentative sequence) (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000  
Accession: S78415  
A:Coltschmidt-Reitsin, S.; Grack, H.R.  
submitted to the Protein Sequence Database, February 1998  
A:Reference number: S78411  
A:Accession: S78415  
A:Molecule type: protein  
A:Residues: 1-16 <GOL>  
A>Note: 1-Val was also found  
A>Note: the protein is designated as mitochondrial ribosomal protein L27  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 23.7%; Score 23.5; DB 2; Length 16;  
Best Local Similarity 46.2%; Pred. No. 1.8e+03;  
Matches 6; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

OY 4 GHERMGRRTSK 16  
DB 1 GADRMK-RTSKR 12

RESULT 19  
JT0610  
leukocyte chemoattractant peptide 9 - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 19-Jan-2001  
C:Accession: JT0610  
R:Murdock, W.J.; McCormick, R.J.  
Biochem. Biophys. Res. Commun. 184, 848-852, 1992  
A:Title: Sequence analysis of leukocyte chemoattractant peptides secreted by perivascular  
A:Reference number: JT0609; MUID:92246975; PMID:1575752  
A:Accession: JT0610  
A:Molecule type: protein  
A:Residues: 1-15 <MOR>  
C:Superfamily: unassigned animal peptides

Query Match 23.2%; Score 23; DB 2; Length 15;  
Best Local Similarity 55.6%; Pred. No. 2e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 VPGHERMGR 10  
DB 5 VAGFGRIGR 13

RESULT 20  
S36891  
ribosomal protein - Mycobacterium bovis (fragment)  
C:Species: Mycobacterium bovis  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
C:Accession: S36891  
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.  
FEBS Lett. 331, 9-14, 1993

A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Myco  
A:Reference number: S36887; MUID:94009653; PMID:8405418  
A:Accession: S36891  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <OHA>

Query Match 23.2%; Score 23; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 2e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 NVPGER 7  
DB 4 NVPANSR 10

RESULT 21  
CA5143  
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 6 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Mar-1998  
C:Accession: CA5143  
R:Yeuung, Y.G.; Berg, K.L.; Pixley, F.J.; Angeletti, R.H.; Stanley, E.R.  
J. Biol. Chem. 267, 23447-23450, 1992  
A:Title: Protein tyrosine phosphatase-1C is rapidly phosphorylated in tyrosine in mac  
A:Reference number: A45143; MUID:93054686; PMID:1385421  
A:Accession: CA5143  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <YEU>  
A:Experimental source: BAC1.2F5 macrophage  
A>Note: sequence extracted from NCBI backbone (NCBI:P118515)  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-pho  
C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 23.2%; Score 23; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NVPGER 6  
DB 3 NIPGXD 8

RESULT 22  
PS0387  
platelet-derived growth factor chain A2 - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-Sep-1993  
C:Accession: PS0387  
R:Nakahara, K.; Nishimura, H.; Kuro-O, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazak  
Biochem. Biophys. Res. Commun. 184, 811-818, 1992  
A:Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vas  
A:Reference number: JN0248; MUID:92246970; PMID:1575749  
A:Accession: PS0387  
A:Molecule type: mRNA  
A:Residues: 1-18 <NAK>  
A>Note: this protein corresponds to the glioma type of human A chain  
C:Superfamily: platelet-derived growth factor

Query Match 23.2%; Score 23; DB 2; Length 18;  
Best Local Similarity 55.6%; Pred. No. 2.4e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 9 GGRRTSKR 17  
DB 1 GRRRESKK 9

RESULT 23  
I50533  
calmodulin - electric eel (fragment)  
C:Species: Electrophorus electricus (electric eel)

Search completed: March 14, 2003, 16:06:29  
Job time : 34 secs

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 29-Sep-1999  
C:Accession: I50533  
R:Munjaal, R.P.; Dedman, J.R.; Means, A.R.  
Ann. N. Y. Acad. Sci. 356, 110-118, 1980  
A:Title: Isolation of the structural gene for calmodulin.  
A:Reference number: I50533; MUID:81205530; PMID:6165309  
A:Accession: I50533  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-22 <MUN>  
A:Cross-references: GB:M25058; NID:9213127; PIDN:AAA62797.1; PID:9213128  
C:Superfamily: calmodulin; calmodulin repeat homology  
C:Keywords: EF hand

Query Match 23.2%; Score 23; DB 2; Length 22;  
Best Local Similarity 38.5%; Pred. No. 3e+03;  
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
6 ERMGGRGTSSKEL 18  
::| | | | |  
2 DKDNGYISAEL 14

RESULT 24  
161239  
heparin-binding epidermal growth factor - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 16-Jul-1999  
C:Accession: I61239  
R:Ren, Z.; Dhadly, M.S.; Yoshizumi, M.; Hilkert, R.J.; Quettermous, T.; Eddy, R.L.; Show  
Biochemistry 32, 7932-7938, 1993  
A:Title: Structural organization and chromosomal assignment of the gene encoding the hum  
A:Reference number: A5313; MUID:93349877; PMID:8347598  
A:Accession: I61239  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-23 <RES>  
A:Cross-references: GB:LI7031; NID:9348173; PIDN:AAA50564.1; PID:9348174  
C:Superfamily: heparin-binding EGF-like growth factor; EGF homology  
C:Keywords: heparin binding

Query Match 23.2%; Score 23; DB 2; Length 23;  
Best Local Similarity 33.3%; Pred. No. 3.1e+03;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
1 NYPGHERMGGRGTSS 15  
:| |::| | |  
8 DVNEEKVKLGWNTS 22

RESULT 25  
178886  
hypothetical Nf-1 ORF3, E73 protein - mouse (fragment)  
C:Species: Mus sp. (mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I78886  
R:Nehls, M.; Pfeiffer, D.; Boehm, T.  
Oncogene 9, 2169-2175, 1994  
A:Title: Exon amplification from complete libraries of genomic DNA using a novel phage v  
A:Reference number: I58399; MUID:94309890; PMID:8036002  
A:Accession: I78886  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-24 <RES>  
A:Cross-references: GB:S71227; NID:9551376; PIDN:AA831327.1; PID:9551377

Query Match 23.2%; Score 23; DB 2; Length 24;  
Best Local Similarity 55.6%; Pred. No. 3.2e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 RMGGRGTSS 15  
| | | | |  
DB 9 RIDGGRPSS 17

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:05:03 ; Search time 15 Seconds  
(without alignments)  
37.269 Million cell updates/sec

Title: US-09-674-913A-1  
Perfect score: 99  
Sequence: 1 NYPGHERMGRGRTSKELA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 147762

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2\_6/prodata2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata2/1aa/PCTus\_COMB.pep:\*  
6: /cgn2\_6/prodata2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	99	100.0	25	2	US-08-726-306A-87
3	47	47.5	10	2	US-08-726-306A-1
4	33.5	33.8	24	4	US-09-540-224-9
5	32	32.3	16	1	US-08-077-797A-34
6	32	32.3	16	5	PCT-US94-01238-34
7	32	32.3	21	5	US-07-841-591A-11
8	32	32.3	21	5	PCT-US93-02034-11
9	32	32.3	24	2	US-09-047-026A-9
10	31	31.3	14	5	PCT-US93-06751-106
11	31	31.3	16	1	US-07-942-245-142
12	31	31.3	20	4	US-09-166-028-3
13	31	31.3	23	4	US-08-874-569B-14
14	31	31.3	24	2	US-09-047-026A-15
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16	30.5	30.8	21	1	US-07-965-667A-10
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23	30	30.3	14	4	US-09-597-877-10
24	29	29.3	10	4	US-08-310-912A-95
25	29	29.3	10	4	US-08-841-089-95
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38	29	29.3	24	2	US-08-706-741B-32	Sequence 32, Appl
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65	27	27.3	24	4	US-09-112-206-69	Sequence 69, Appl
66	27	27.3	25	4	US-09-292-225-23	Sequence 23, Appl
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102	26	26.3	21	4	US-08-470-335-30	Sequence 30, App1	175	24.5	24.7	8	5	PCT-US93-10197-1	Sequence 2, App1
103	26	26.3	21	4	US-08-735-021-30	Sequence 30, App1	176	24	24.2	21	1	US-08-153-855-2	Sequence 1, App1
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106	26	26.3	21	4	US-09-173-480-4	Sequence 4, App1	179	24	24.2	10	1	US-08-445-745-105	Sequence 105, App
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110	26	26.3	21	5	PCT-US95-06846A-30	Sequence 30, App1	183	24	24.2	10	3	US-09-139-762A-39	Sequence 39, App1
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112	26	26.3	22	1	US-08-441-914-10	Sequence 10, App1	185	24	24.2	10	4	US-09-074-658-57	Sequence 57, App1
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129	25	25.3	11	4	US-09-189-344-20	Sequence 20, App1	202	24	24.2	12	4	US-08-469-260A-501	Sequence 501, App
130	25	25.3	11	4	US-08-981-392-39	Sequence 39, App1	203	24	24.2	12	5	PCT-US95-05471-60	Sequence 60, App1
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138	25	25.3	14	2	US-08-473-025-6	Sequence 6, App1	211	24	24.2	14	5	US-08-182-967-21	Sequence 24, App1
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142	25	25.3	16	2	US-08-124-981A-27	Sequence 27, App1	215	24	24.2	15	1	US-08-073-884C-29	Sequence 29, App1
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254	24	24.2	20	4	US-09-101-135-6	Sequence 10, Appl	327	23	23.2	15	4	US-09-248-574A-4	Sequence 4, Appl
255	24	24.2	20	4	US-08-818-252-10	Sequence 4, Appl	328	23	23.2	15	4	US-09-381-601-3	Sequence 4, Appl
256	24	24.2	20	4	US-08-842-322-4	Sequence 26, Appl	329	23	23.2	15	4	US-08-992-877-10	Sequence 10, Appl
257	24	24.2	20	4	US-09-316-919-26	Sequence 2, Appl	330	23	23.2	15	4	US-09-929-962-4	Sequence 4, Appl
258	24	24.2	22	1	US-08-039-778B-2	Sequence 5, Appl	331	23	23.2	15	5	US-09-503-632-4	Sequence 68, Appl
259	24	24.2	22	1	US-08-039-778B-5	Sequence 16, Appl	332	23	23.2	16	1	US-07-942-245-52	Sequence 52, Appl
260	24	24.2	22	4	US-07-946-180B-16	Sequence 218, App	333	23	23.2	16	1	US-07-942-245-53	Sequence 53, Appl
261	24	24.2	22	4	US-09-556-877-218	Sequence 218, App	334	23	23.2	16	1	US-07-942-245-66	Sequence 66, Appl
262	24	24.2	22	6	5182262-10	Patent No. 5182262	335	23	23.2	16	1	US-07-942-245-66	Sequence 148, App
263	24	24.2	22	6	5182262-10	Patent No. 5182262	336	23	23.2	16	1	US-07-942-245-148	Sequence 5, Appl
264	24	24.2	22	6	5182262-10	Patent No. 5182262	337	23	23.2	16	1	US-08-448-600-5	Sequence 207, App
265	24	24.2	22	6	5182262-10	Patent No. 5182262	338	23	23.2	16	2	US-08-752-852A-207	Sequence 9, Appl
266	24	24.2	22	6	5433940-9	Patent No. 5433940	339	23	23.2	16	3	US-08-937-610-9	Sequence 179, App
267	24	24.2	23	1	US-08-176-500-89	Sequence 89, Appl	340	23	23.2	17	4	US-08-469-260A-179	Sequence 2, Appl
268	24	24.2	23	1	US-08-471-052A-89	Sequence 89, Appl	341	23	23.2	17	4	US-08-468-674B-13	Sequence 13, Appl
269	24	24.2	23	1	US-08-189-331-89	Sequence 89, Appl	342	23	23.2	18	1	US-08-704-170-33	Sequence 33, Appl
270	24	24.2	23	2	US-08-471-939-89	Sequence 89, Appl	343	23	23.2	18	1	US-08-634-060-54	Sequence 54, Appl
271	24	24.2	23	2	US-08-471-800-89	Sequence 89, Appl	344	23	23.2	18	1	US-08-780-571-13	Sequence 13, Appl
272	24	24.2	23	2	US-08-471-068-89	Sequence 8, Appl	345	23	23.2	18	1	US-08-685-589A-214	Sequence 214, App
273	24	24.2	23	4	US-09-736-915-8	Sequence 19, Appl	346	23	23.2	18	2	US-08-476-866-22	Sequence 22, Appl
274	24	24.2	24	4	US-09-297-981-19	Sequence 12, Appl	347	23	23.2	18	2	US-09-467-997-9	Sequence 9, Appl
275	24	24.2	24	4	US-09-028-937-12	Sequence 4, Appl	348	23	23.2	18	4	US-08-469-260A-302	Sequence 302, App
276	24	24.2	25	2	US-08-146-028-17	Sequence 17, Appl	349	23	23.2	18	4	US-09-321-932B-39	Sequence 39, Appl
277	24	24.2	25	2	US-08-146-028-163	Sequence 163, App	350	23	23.2	18	5	PCF-US93-05325-12	Sequence 12, Appl
278	24	24.2	25	2	US-08-192-553-25	Sequence 25, Appl	351	23	23.2	18	5	PCF-US93-06751-139	Sequence 139, App
279	24	24.2	25	4	US-08-723-425A-17	Sequence 17, Appl	352	23	23.2	19	5	PCF-US94-02631-33	Sequence 33, Appl
280	24	24.2	25	4	US-08-723-425A-163	Sequence 163, App	353	23	23.2	19	5	US-08-347-000-103	Sequence 103, Appl
281	24	24.2	25	4	US-09-112-206-17	Sequence 17, Appl	354	23	23.2	19	4	US-09-169-015-52	Sequence 52, Appl
282	24	24.2	25	4	US-09-112-206-163	Sequence 163, App	355	23	23.2	19	4	US-09-381-601-31	Sequence 31, Appl
283	24	24.2	25	4	US-09-381-601-6	Sequence 6, Appl	356	23	23.2	19	4	US-08-871-561-39	Sequence 39, Appl
284	23	23.7	16	4	US-09-227-357-520	Sequence 24, Appl	357	23	23.2	19	4	US-09-620-0132C-249	Sequence 249, App
285	23	23.5	23	4	US-08-733-982A-13	Sequence 520, App	358	23	23.2	19	5	PCF-US92-07865-9	Sequence 9, Appl
286	23	23.7	8	2	US-08-529-190B-21	Sequence 21, Appl	359	23	23.2	19	5	PCF-US95-03236-15	Sequence 15, Appl
287	23	23.2	10	2	US-08-406-330-18	Sequence 18, Appl	360	23	23.2	20	5	PCF-US93-05325-11	Sequence 11, Appl
288	23	23.2	10	2	US-08-406-330-21	Sequence 21, Appl	361	23	23.2	20	1	US-07-700-526-15	Sequence 58, Appl
289	23	23.2	10	2	US-08-556-597-18	Sequence 18, Appl	362	23	23.2	20	1	US-08-418-893D-5	Sequence 5, Appl
290	23	23.2	10	2	US-08-556-597-21	Sequence 21, Appl	363	23	23.2	20	1	US-08-208-181A-8	Sequence 8, Appl
291	23	23.2	10	2	US-08-556-597-21	Sequence 21, Appl	364	23	23.2	20	1	US-08-208-181A-10	Sequence 10, Appl
292	23	23.2	10	2	US-08-556-597-21	Sequence 21, Appl	365	23	23.2	20	3	US-08-523-373-1	Sequence 1, Appl
293	23	23.2	10	3	US-08-482-228-202	Sequence 202, App	366	23	23.2	20	4	US-08-602-999A-140	Sequence 140, App
294	23	23.2	10	3	US-08-482-528-202	Sequence 614, App	367	23	23.2	20	4	US-09-556-877-249	Sequence 249, App
295	23	23.2	11	4	US-08-469-260A-521	Sequence 521, App	368	23	23.2	20	4	US-09-500-124-140	Sequence 140, App
296	23	23.2	12	1	US-08-413-681A-15	Sequence 15, Appl	369	23	23.2	20	4	US-09-620-0132C-249	Sequence 249, App
297	23	23.2	12	1	US-08-260-582-45	Sequence 45, Appl	370	23	23.2	20	5	PCF-US92-03132-15	Sequence 15, App
298	23	23.2	12	1	US-08-260-582-56	Sequence 56, Appl	371	23	23.2	20	5	PCF-US93-05325-11	Sequence 11, Appl
299	23	23.2	12	1	US-08-454-097-50	Sequence 50, Appl	372	23	23.2	20	5	PCF-US93-05325-11	Sequence 11, Appl
300	23	23.2	12	1	US-08-454-097-51	Sequence 51, Appl	373	23	23.2	21	3	US-08-256-747C-32	Sequence 32, Appl
301	23	23.2	12	2	US-08-811-492-141	Sequence 141, App	374	23	23.2	21	4	US-09-024-975-11	Sequence 11, Appl
302	23	23.2	12	3	US-08-185-359-50	Sequence 50, Appl	375	23	23.2	21	4	US-08-834-130A-32	Sequence 32, Appl
303	23	23.2	12	3	US-08-185-359-51	Sequence 51, Appl	376	23	23.2	22	1	US-08-264-002-12	Sequence 12, Appl
304	23	23.2	12	3	US-09-322-911-15	Sequence 15, Appl	377	23	23.2	22	2	US-08-701-124-53	Sequence 53, Appl
305	23	23.2	12	5	US-08-687-590-5	Sequence 5, Appl	378	23	23.2	22	2	US-08-969-721-3	Sequence 3, Appl
306	23	23.2	12	5	PCF-US93-05701-13	Sequence 13, Appl	379	23	23.2	22	2	US-08-969-721-10	Sequence 10, Appl
307	23	23.2	12	5	PCF-US95-05471-45	Sequence 45, Appl	380	23	23.2	22	2	US-08-896-176-3	Sequence 3, Appl
308	23	23.2	12	5	PCF-US95-05471-45	Sequence 56, Appl	381	23	23.2	22	4	US-09-130-225-53	Sequence 53, Appl
309	23	23.2	12	6	PCF-US95-05471-45	Sequence 56, Appl	382	23	23.2	22	4	US-09-455-061-53	Sequence 53, Appl
310	23	23.2	13	4	US-08-444-818-129	Sequence 129, App	383	23	23.2	23	2	US-08-850-910A-27	Sequence 27, Appl
311	23	23.2	13	4	US-09-306-059-25	Sequence 25, Appl	384	23	23.2	24	1	US-07-748-344B-3	Sequence 3, Appl
312	23	23.2	13	6	US-09-206-059-28	Sequence 28, Appl	385	23	23.2	24	1	US-08-657-182-10	Sequence 10, Appl
313	23	23.2	14	3	US-08-637-759B-214	Sequence 214, App	386	23	23.2	24	2	US-08-465-794-1	Sequence 3, Appl
314	23	23.2	14	3	US-08-871-335A-214	Sequence 214, App	387	23	23.2	24	2	US-08-954-965A-3	Sequence 3, Appl
315	23	23.2	14	4	US-08-433-613-15	Sequence 15, App	388	23	23.2	24	2	US-09-047-026A-8	Sequence 8, Appl
316	23	23.2	14	4	US-09-248-574A-1	Sequence 1, Appl	389	23	23.2	24	3	US-09-049-813-1	Sequence 1, Appl
317	23	23.2	14	4	US-09-201-945-214	Sequence 214, App	390	23	23.2	24	3	US-08-256-747C-67	Sequence 67, Appl
318	23	23.2	14	4	US-09-201-945-214	Sequence 214, App	391	23	23.2	24	3	US-08-834-130A-67	Sequence 67, Appl
319	23	23.2	14	4	US-09-929-962-1	Sequence 1, Appl	392	23	23.2	24	4	US-08-834-130A-67	Sequence 67, Appl

393	23	23.2	24	4	US-09-400-208B-3	Sequence 3, Appl1	466	22	22.2	15	2	US-08-733-982A-14	Sequence 14, Appl1
394	23	23.2	24	4	US-08-137-08B-3	Sequence 3, Appl1	467	22	22.2	15	2	US-08-933-402-122	Sequence 122, App
395	23	23.2	24	6	5171680-13	Patent No. 5171680	468	22	22.2	15	2	US-09-207-621-122	Sequence 122, App
396	23	23.2	25	1	US-07-748-344B-1	Sequence 1, Appl1	469	22	22.2	15	2	US-08-532-818-122	Sequence 122, App
397	23	23.2	25	2	US-08-621-564B-2	Sequence 2, Appl1	470	22	22.2	15	2	US-08-752-852A-119	Sequence 199, App
398	23	23.2	25	2	US-08-473-475A-6	Sequence 6, Appl1	471	22	22.2	15	3	US-09-231-797-122	Sequence 122, App
399	23	23.2	25	2	US-08-997-080-64	Sequence 64, Appl1	472	22	22.2	15	3	US-08-934-224-122	Sequence 122, App
400	23	23.2	25	2	US-08-954-985A-1	Sequence 1, Appl1	473	22	22.2	15	3	US-08-933-843-122	Sequence 122, App
401	23	23.2	25	2	US-08-997-362-64	Sequence 64, Appl1	474	22	22.2	15	3	US-08-469-141A-11	Sequence 11, Appl1
402	23	23.2	25	3	US-08-873-970-64	Sequence 64, Appl1	475	22	22.2	15	4	US-08-934-223-122	Sequence 122, App
403	23	23.2	25	3	US-09-095-855-64	Sequence 64, Appl1	476	22	22.2	15	4	US-08-706-391A-8	Sequence 8, Appl1
404	23	23.2	25	4	US-09-381-601-5	Sequence 5, Appl1	477	22	22.2	15	4	US-08-602-999A-345	Sequence 345, App
405	23	23.2	25	4	US-09-324-542-64	Sequence 64, Appl1	478	22	22.2	15	4	US-09-413-492-122	Sequence 122, App
406	23	23.2	25	4	US-09-205-426-64	Sequence 64, Appl1	479	22	22.2	15	4	US-08-997-251-6	Sequence 6, Appl1
407	23	23.2	25	4	US-08-137-08B-1	Sequence 1, Appl1	480	22	22.2	15	4	US-08-630-915A-171	Sequence 171, App
408	22.5	22.7	13	1	US-08-484-184-3	Sequence 3, Appl1	481	22	22.2	15	4	US-09-500-124-345	Sequence 345, App
409	22.5	22.7	13	1	US-08-087-219-3	Sequence 3, Appl1	482	22	22.2	15	4	US-09-561-490E-9	Sequence 9, Appl1
410	22.5	22.7	13	1	US-08-269-929-7	Sequence 7, Appl1	483	22	22.2	15	4	PCT-US93-06751-6	Sequence 6, Appl1
411	22.5	22.7	16	4	US-09-297-981-28	Sequence 7, Appl1	484	22	22.2	15	5	PCT-US93-06751-7	Sequence 7, Appl1
412	22.5	22.7	19	4	US-09-106-568B-91	Sequence 28, Appl1	485	22	22.2	15	5	PCT-US93-06751-32	Sequence 32, Appl1
413	22.5	22.7	22	1	US-07-698-928A-5	Sequence 91, Appl1	486	22	22.2	15	5	PCT-US93-06751-52	Sequence 52, Appl1
414	22.5	22.7	22	4	US-09-127-815D-36	Sequence 5, Appl1	487	22	22.2	15	5	PCT-US93-06751-86	Sequence 86, Appl1
415	22.2	22.2	5	3	US-08-985-526-17	Sequence 36, Appl1	488	22	22.2	15	5	PCT-US95-1379A-11	Sequence 11, Appl1
416	22	22.2	5	4	US-08-290-995-3	Sequence 17, Appl1	489	22	22.2	16	1	US-08-447-925-5	Sequence 5, Appl1
417	22	22.2	5	4	US-08-264-002-13	Sequence 3, Appl1	490	22	22.2	16	1	US-07-942-245-65	Sequence 65, Appl1
418	22	22.2	8	4	US-08-635-928-15	Sequence 13, Appl1	491	22	22.2	16	1	US-07-942-245-70	Sequence 70, Appl1
419	22	22.2	8	4	US-08-817-441-24	Sequence 15, Appl1	492	22	22.2	16	1	US-07-942-245-99	Sequence 99, Appl1
420	22	22.2	8	6	5204259-20	Patent No. 5204259	493	22	22.2	16	1	US-07-942-245-104	Sequence 104, App
421	22	22.2	9	1	US-08-454-207A-70	Sequence 70, Appl1	494	22	22.2	16	1	US-07-942-245-103	Sequence 103, App
422	22	22.2	9	1	US-08-615-181-90	Sequence 90, Appl1	495	22	22.2	16	1	US-07-942-245-113	Sequence 113, App
423	22	22.2	9	2	US-08-704-655-24	Sequence 24, Appl1	496	22	22.2	16	1	US-08-257-528B-73	Sequence 73, App
424	22	22.2	9	3	US-09-162-368B-24	Sequence 24, Appl1	497	22	22.2	16	1	US-08-182-483A-20	Sequence 20, Appl1
425	22	22.2	9	4	US-09-161-877B-24	Sequence 24, Appl1	498	22	22.2	16	1	US-08-243-879A-19	Sequence 19, Appl1
426	22	22.2	9	4	US-09-675-922-27	Sequence 27, Appl1	499	22	22.2	16	1	US-08-460-602A-73	Sequence 73, Appl1
427	22	22.2	10	1	US-08-300-386A-56	Sequence 26, Appl1	500	22	22.2	16	1	US-08-465-217A-73	Sequence 73, Appl1
428	22	22.2	10	2	US-09-016-366A-56	Sequence 26, Appl1	501	22	22.2	16	1	US-08-465-167A-73	Sequence 73, Appl1
429	22	22.2	10	2	US-08-978-404B-35	Sequence 35, Appl1	502	22	22.2	16	1	US-08-499-523-40	Sequence 40, Appl1
430	22	22.2	10	3	US-08-159-339A-669	Sequence 69, Appl1	503	22	22.2	16	2	US-08-464-329A-73	Sequence 73, Appl1
431	22	22.2	10	3	US-08-931-645-56	Sequence 56, Appl1	504	22	22.2	16	2	US-08-615-942A-9	Sequence 9, Appl1
432	22	22.2	10	4	US-09-330-548-5	Sequence 5, Appl1	505	22	22.2	16	2	US-08-462-507A-73	Sequence 73, Appl1
433	22	22.2	10	5	PCT-US94-01258-56	Sequence 56, Appl1	506	22	22.2	16	2	US-08-467-881A-73	Sequence 73, Appl1
434	22	22.2	10	5	PCT-US95-11235-56	Sequence 56, Appl1	507	22	22.2	16	4	US-09-128-345-40	Sequence 40, Appl1
435	22	22.2	10	6	5204259-11	Patent No. 5204259	508	22	22.2	16	4	US-08-602-999A-211	Sequence 211, App
436	22	22.2	11	2	US-08-669-721-16	Sequence 16, Appl1	509	22	22.2	16	4	US-09-488-799-5	Sequence 5, Appl1
437	22	22.2	11	3	US-09-075-257A-19	Sequence 19, Appl1	510	22	22.2	16	4	US-09-230-548-17	Sequence 17, Appl1
438	22	22.2	11	4	US-08-836-075A-116	Sequence 116, Appl1	511	22	22.2	16	4	US-09-500-124-211	Sequence 211, App
439	22	22.2	11	4	US-09-189-344-16	Sequence 16, Appl1	512	22	22.2	17	2	US-09-115-209-69	Sequence 69, Appl1
440	22	22.2	11	4	US-09-534-639-19	Sequence 19, Appl1	513	22	22.2	17	4	US-08-990-823-101	Sequence 101, App
441	22	22.2	11	4	US-09-297-981-18	Sequence 18, Appl1	514	22	22.2	18	1	US-08-061-350-4	Sequence 1, Appl1
442	22	22.2	11	6	5223254-12	Patent No. 5223254	515	22	22.2	18	1	US-08-553-110-1	Sequence 1, Appl1
443	22	22.2	12	1	US-07-854-629-7	Sequence 7, Appl1	516	22	22.2	18	2	US-08-224-591-10	Sequence 10, Appl1
444	22	22.2	12	1	US-08-474-008-7	Sequence 7, Appl1	517	22	22.2	18	2	US-08-819-033-3	Sequence 3, Appl1
445	22	22.2	12	2	US-08-811-492-134	Sequence 134, Appl1	518	22	22.2	18	2	US-08-649-991-51	Sequence 51, Appl1
446	22	22.2	12	2	US-08-564-972-73	Sequence 73, Appl1	519	22	22.2	18	2	US-08-926-789-10	Sequence 10, Appl1
447	22	22.2	12	3	US-08-816-346-34	Sequence 34, Appl1	520	22	22.2	18	2	US-08-818-253-45	Sequence 45, Appl1
448	22	22.2	12	4	US-09-335-411-34	Sequence 34, Appl1	521	22	22.2	18	3	US-08-946-026-50	Sequence 50, Appl1
449	22	22.2	12	4	US-09-258-754-95	Sequence 95, Appl1	522	22	22.2	18	4	US-09-070-637-13	Sequence 13, Appl1
450	22	22.2	12	4	US-09-042-107-95	Sequence 95, Appl1	523	22	22.2	18	4	US-08-818-352-45	Sequence 45, Appl1
451	22	22.2	12	4	US-09-518-046-34	Sequence 34, Appl1	524	22	22.2	18	4	US-09-362-805-7	Sequence 7, Appl1
452	22	22.2	12	4	US-09-297-981-30	Sequence 30, Appl1	525	22	22.2	18	4	US-09-173-190-7	Sequence 7, Appl1
453	22	22.2	14	1	US-08-471-780C-89	Sequence 89, Appl1	526	22	22.2	18	4	US-09-069-821-10	Sequence 10, Appl1
454	22	22.2	14	1	US-08-467-282B-89	Sequence 89, Appl1	527	22	22.2	18	4	US-09-316-919-61	Sequence 61, Appl1
455	22	22.2	14	2	US-08-471-282A-89	Sequence 89, Appl1	528	22	22.2	18	5	PCT-US94-01234-9	Sequence 10, Appl1
456	22	22.2	14	2	US-08-466-710C-89	Sequence 89, Appl1	529	22	22.2	18	5	PCT-US94-01234-9	Sequence 9, Appl1
457	22	22.2	14	3	US-08-468-739C-89	Sequence 89, Appl1	530	22	22.2	19	1	US-08-492-599-2	Sequence 2, Appl1
458	22	22.2	14	4	US-08-687-590-44	Sequence 44, Appl1	531	22	22.2	19	1	US-08-492-599-3	Sequence 3, Appl1
459	22	22.2	14	4	US-08-687-590-47	Sequence 44, Appl1	532	22	22.2	19	2	US-08-975-699-16	Sequence 16, Appl1
460	22	22.2	14	5	PCT-US93-06751-74	Sequence 74, Appl1	533	22	22.2	19	4	US-08-972-089-16	Sequence 16, Appl1
461	22	22.2	14	5	PCT-US93-06751-77	Sequence 77, Appl1	534	22	22.2	19	4	US-09-166-028-1	Sequence 1, Appl1
462	22	22.2	15	1	US-07-805-437-8	Sequence 8, Appl1	535	22	22.2	19	4	US-08-628-829-23	Sequence 23, Appl1
463	22	22.2	15	1	US-07-969-336-1	Sequence 1, Appl1	536	22	22.2	19	4	US-09-297-981-16	Sequence 16, Appl1
464	22	22.2	15	2	US-08-815-953-1	Sequence 122, App	537	22	22.2	19	4	US-09-210-422-15	Sequence 15, Appl1
465	22	22.2	15	2	US-08-934-222-122	Sequence 122, App	538	22	22.2	19	5	PCT-US96-10455-2	Sequence 2, Appl1

539	22	22.2	19	5	PCT-US96-10455-3	Sequence 3, Appl	612	21	21.2	7	4	US-09-173-941-10	Sequence 10, Appl
540	22	22.2	20	1	US-08-066-309-3	Sequence 3, Appl	613	21	21.2	7	4	US-09-173-941-61	Sequence 61, Appl
541	22	22.2	20	1	US-08-218-608-7	Sequence 7, Appl	614	21	21.2	7	4	US-09-173-941-63	Sequence 63, Appl
542	22	22.2	20	2	US-08-564-972-43	Sequence 43, Appl	615	21	21.2	7	4	US-09-173-941-73	Sequence 73, Appl
543	22	22.2	20	2	US-08-564-972-44	Sequence 44, Appl	616	21	21.2	7	4	US-08-640-737-35	Sequence 35, Appl
544	22	22.2	20	2	US-08-240-717A-2	Sequence 2, Appl	617	21	21.2	8	2	US-08-318-837-30	Sequence 30, Appl
545	22	22.2	20	3	US-08-504-538A-3	Sequence 3, Appl	618	21	21.2	8	2	US-08-810-712-19	Sequence 19, Appl
546	22	22.2	20	4	US-08-861-338-4	Sequence 4, Appl	619	21	21.2	8	6	5175147-10	Patent No. 5175147
547	22	22.2	20	4	US-08-160-604-127	Sequence 127, App	620	21	21.2	9	1	US-08-469-582-14	Sequence 14, Appl
548	22	22.2	20	4	US-09-249-458A-3	Sequence 3, Appl	621	21	21.2	9	1	US-08-615-181-46	Sequence 46, Appl
549	22	22.2	20	4	US-08-290-736C-45	Sequence 45, Appl	622	21	21.2	9	2	US-08-704-655-23	Sequence 23, Appl
550	22	22.2	20	4	US-08-630-052-3	Sequence 3, Appl	623	21	21.2	9	4	US-09-644-600-62	Sequence 62, Appl
551	22	22.2	20	4	US-09-556-877-246	Sequence 246, App	624	21	21.2	10	1	US-08-445-745-52	Sequence 52, Appl
552	22	22.2	20	4	US-09-620-412C-246	Sequence 246, App	625	21	21.2	10	1	US-08-445-745-58	Sequence 58, Appl
553	22	22.2	20	5	PCT-US94-05660-3	Sequence 3, Appl	626	21	21.2	10	1	US-08-445-745-104	Sequence 104, Appl
554	22	22.2	20	5	PCT-US95-09307-3	Sequence 3, Appl	627	21	21.2	10	1	US-08-445-745-107	Sequence 107, App
555	22	22.2	21	1	US-08-127-499A-2	Sequence 2, Appl	628	21	21.2	10	1	US-08-445-745-108	Sequence 108, App
556	22	22.2	21	1	US-08-482-847-2	Sequence 2, Appl	629	21	21.2	10	1	US-08-469-582-11	Sequence 11, Appl
557	22	22.2	21	2	US-08-480-190-272	Sequence 272, App	630	21	21.2	10	1	US-08-704-170-27	Sequence 27, Appl
558	22	22.2	21	2	US-08-488-379-272	Sequence 272, App	631	21	21.2	10	1	US-08-218-026-13	Sequence 66, Appl
559	22	22.2	21	2	US-08-485-937-7	Sequence 7, Appl	632	21	21.2	10	1	US-08-218-026-15	Sequence 13, Appl
560	22	22.2	21	2	US-08-373-215-7	Sequence 7, Appl	633	21	21.2	10	2	US-08-653-632-13	Sequence 13, Appl
561	22	22.2	21	4	US-09-057-897-31	Sequence 31, Appl	634	21	21.2	10	2	US-08-653-632-15	Sequence 15, Appl
562	22	22.2	21	5	PCT-US93-06552-7	Sequence 7, Appl	635	21	21.2	10	2	US-08-556-597-134	Sequence 134, App
563	22	22.2	21	5	PCT-US93-07545-272	Sequence 7, App	636	21	21.2	10	2	US-08-556-597-172	Sequence 172, App
564	22	22.2	22	1	US-08-678-444-1	Sequence 1, Appl	637	21	21.2	10	2	US-08-769-745-3	Sequence 3, Appl
565	22	22.2	22	1	US-08-484-635-174	Sequence 174, App	638	21	21.2	10	3	US-08-997-5328-2	Sequence 2, Appl
566	22	22.2	22	2	US-08-484-631-174	Sequence 174, App	639	21	21.2	10	4	US-09-306-756-1	Sequence 1, Appl
567	22	22.2	22	2	US-08-248-839C-73	Sequence 73, App	640	21	21.2	10	4	US-09-194-062-12	Sequence 12, Appl
568	22	22.2	22	2	US-08-827-570-174	Sequence 174, App	641	21	21.2	10	4	US-08-456-466-1	Sequence 1, Appl
569	22	22.2	22	2	US-08-751-767A-78	Sequence 78, Appl	642	21	21.2	10	4	US-08-456-466-28	Sequence 28, Appl
570	22	22.2	22	3	US-08-985-526-19	Sequence 19, Appl	643	21	21.2	10	4	US-08-456-466-35	Sequence 35, Appl
571	22	22.2	22	3	US-09-100-409A-52	Sequence 52, Appl	644	21	21.2	10	4	US-08-456-466-82	Sequence 82, Appl
572	22	22.2	22	4	US-08-469-260A-558	Sequence 558, App	645	21	21.2	10	4	US-08-456-466-85	Sequence 85, Appl
573	22	22.2	22	5	PCT-US92-08094-6	Sequence 6, Appl	646	21	21.2	10	4	US-08-456-466-86	Sequence 86, Appl
574	22	22.2	23	1	US-08-112-208C-21	Sequence 21, Appl	647	21	21.2	10	5	PCT-US94-02631-27	Sequence 27, Appl
575	22	22.2	23	1	US-08-248-819A-23	Sequence 23, Appl	648	21	21.2	10	5	PCT-US94-02631-66	Sequence 66, Appl
576	22	22.2	23	2	US-08-337-646A-41	Sequence 41, Appl	650	21	21.2	10	5	PCT-US95-03236-6	Sequence 6, Appl
577	22	22.2	23	2	US-08-856-531-21	Sequence 21, Appl	651	21	21.2	11	1	US-08-217-188A-51	Sequence 51, Appl
578	22	22.2	23	4	US-08-856-034-21	Sequence 21, Appl	652	21	21.2	11	1	US-08-469-582-10	Sequence 10, Appl
579	22	22.2	23	4	US-09-029-348-8	Sequence 8, Appl	653	21	21.2	11	1	US-08-476-405A-27	Sequence 27, Appl
580	22	22.2	23	4	US-08-927-326-41	Sequence 41, Appl	654	21	21.2	11	1	US-08-687-226-51	Sequence 51, Appl
581	22	22.2	23	4	US-09-585-887-2	Sequence 2, Appl	655	21	21.2	11	1	US-08-218-026-43	Sequence 43, Appl
582	22	22.2	23	4	US-09-289-578-2	Sequence 2, Appl	656	21	21.2	11	2	US-08-342-930-4	Sequence 4, Appl
583	22	22.2	23	4	US-09-125-138-4	Sequence 4, Appl	657	21	21.2	11	2	US-08-653-632-43	Sequence 43, Appl
584	22	22.2	24	2	US-08-306-078-6	Sequence 6, Appl	658	21	21.2	11	2	US-08-669-721-19	Sequence 19, Appl
585	22	22.2	24	2	US-09-047-026A-12	Sequence 12, Appl	659	21	21.2	11	2	US-08-473-025-7	Sequence 7, Appl
586	22	22.2	24	3	US-08-504-558A-8	Sequence 8, Appl	660	21	21.2	11	3	US-08-667-725B-51	Sequence 51, Appl
587	22	22.2	24	4	US-09-249-458A-8	Sequence 8, Appl	661	21	21.2	11	4	US-09-007-748-51	Sequence 51, Appl
588	22	22.2	24	4	US-09-230-548-27	Sequence 27, Appl	662	21	21.2	11	4	US-09-189-344-19	Sequence 19, Appl
589	22	22.2	24	4	US-09-227-357-524	Sequence 524, App	663	21	21.2	11	4	US-09-206-059-17	Sequence 17, Appl
590	22	22.2	24	4	US-09-043-731-20	Sequence 20, Appl	664	21	21.2	11	4	US-09-027-108C-4	Sequence 4, Appl
591	22	22.2	24	4	US-08-630-052-8	Sequence 8, Appl	665	21	21.2	12	1	US-08-260-582-55	Sequence 55, Appl
592	22	22.2	24	5	PCT-US95-09307-8	Sequence 8, Appl	666	21	21.2	12	1	US-08-469-582-20	Sequence 20, Appl
593	22	22.2	25	1	US-07-754-918A-3	Sequence 3, Appl	667	21	21.2	12	1	US-08-469-582-21	Sequence 21, Appl
594	22	22.2	25	1	US-08-248-839C-184	Sequence 184, App	668	21	21.2	12	1	US-08-671-525B-15	Sequence 15, Appl
595	22	22.2	25	4	US-09-025-596-38	Sequence 38, Appl	669	21	21.2	12	1	US-08-671-525B-20	Sequence 20, Appl
596	21.5	21.7	25	4	US-08-395-602A-3	Sequence 3, Appl	670	21	21.2	12	1	US-08-671-525B-22	Sequence 22, Appl
597	21.5	21.7	23	4	US-08-021-625D-3	Sequence 3, Appl	671	21	21.2	12	1	US-08-671-525B-23	Sequence 23, Appl
598	21.5	21.7	24	2	US-09-392-277-28	Sequence 28, Appl	672	21	21.2	12	1	US-08-671-525B-23	Sequence 23, Appl
599	21	21.2	5	3	US-08-941-532-3	Sequence 3, Appl	673	21	21.2	12	1	US-08-672-109B-15	Sequence 15, Appl
600	21	21.2	5	4	US-09-006-428A-22	Sequence 22, Appl	674	21	21.2	12	1	US-08-672-109B-20	Sequence 20, Appl
601	21	21.2	6	1	US-07-634-634B-1	Sequence 1, Appl	675	21	21.2	12	1	US-08-672-109B-21	Sequence 21, Appl
602	21	21.2	6	3	US-08-482-528-145	Sequence 145, App	676	21	21.2	12	1	US-08-672-109B-22	Sequence 22, Appl
603	21	21.2	6	3	US-08-482-528-145	Sequence 145, App	677	21	21.2	12	1	US-08-672-109B-23	Sequence 23, Appl
604	21	21.2	6	3	US-08-941-532-2	Sequence 2, Appl	678	21	21.2	12	1	US-08-548-540-155	Sequence 155, App
605	21	21.2	6	3	US-08-513-968-61	Sequence 61, Appl	679	21	21.2	12	1	US-08-191-338A-12	Sequence 12, Appl
606	21	21.2	6	4	US-09-020-880-55	Sequence 55, Appl	680	21	21.2	12	2	US-08-842-045-15	Sequence 15, Appl
607	21	21.2	6	4	US-08-635-928-13	Sequence 13, Appl	681	21	21.2	12	2	US-08-842-045-20	Sequence 20, Appl
608	21	21.2	6	4	US-09-101-544-55	Sequence 55, Appl	682	21	21.2	12	2	US-08-842-045-21	Sequence 21, Appl
609	21	21.2	7	1	US-09-006-428A-21	Sequence 21, Appl	683	21	21.2	12	2	US-08-842-045-22	Sequence 22, Appl
610	21	21.2	7	1	US-08-545-228-1	Sequence 1, Appl	684	21	21.2	12	2	US-08-842-045-23	Sequence 23, Appl
611	21	21.2	7	2	US-08-776-585-12	Sequence 12, Appl							

685	21	21.2	12	2	US-08-842-238-15	Sequence 15, Appl	758	21	21.2	15	2	US-07-847-311A-8	Sequence 8, Appl
686	21	21.2	12	2	US-08-842-238-20	Sequence 20, Appl	759	21	21.2	15	2	US-08-986-234-23	Sequence 23, Appl
687	21	21.2	12	2	US-08-842-238-21	Sequence 21, Appl	760	21	21.2	15	4	US-08-930-917A-9	Sequence 9, Appl
688	21	21.2	12	2	US-08-842-238-22	Sequence 22, Appl	761	21	21.2	15	4	US-08-604-365-30	Sequence 30, Appl
689	21	21.2	12	2	US-08-842-238-23	Sequence 23, Appl	762	21	21.2	15	4	US-09-035-098-3	Sequence 3, Appl
690	21	21.2	12	2	US-08-637-759B-407	Sequence 407, App	763	21	21.2	15	4	US-08-060-988A-42	Sequence 42, Appl
691	21	21.2	12	2	US-08-538-711A-2	Sequence 2, Appl1	764	21	21.2	15	5	PCT-US93-06751-25	Sequence 25, Appl
692	21	21.2	12	3	US-08-871-355A-407	Sequence 407, App	765	21	21.2	15	5	PCT-US93-06751-48	Sequence 48, Appl
693	21	21.2	12	3	US-08-629-335B-15	Sequence 15, Appl	766	21	21.2	15	5	PCT-US93-06751-75	Sequence 75, Appl
694	21	21.2	12	3	US-08-629-335B-20	Sequence 20, Appl	767	21	21.2	15	5	PCT-US93-06751-107	Sequence 107, App
695	21	21.2	12	3	US-08-629-335B-21	Sequence 21, Appl	768	21	21.2	15	5	PCT-US95-04018-23	Sequence 23, Appl
696	21	21.2	12	3	US-08-629-335B-22	Sequence 22, Appl	769	21	21.2	16	1	US-08-053-616-4	Sequence 4, Appl
697	21	21.2	12	3	US-08-629-335B-23	Sequence 23, Appl	770	21	21.2	16	1	US-07-994-469A-21	Sequence 21, Appl
698	21	21.2	12	4	US-09-258-754-88	Sequence 88, Appl	771	21	21.2	16	1	US-07-994-657-3	Sequence 3, Appl
699	21	21.2	12	4	US-09-042-107-88	Sequence 88, Appl	772	21	21.2	16	1	US-07-942-245-95	Sequence 95, Appl
700	21	21.2	12	4	US-08-725-027-2	Sequence 2, Appl1	773	21	21.2	16	1	US-07-942-245-96	Sequence 96, Appl
701	21	21.2	12	4	US-09-201-945-407	Sequence 407, App	774	21	21.2	16	1	US-07-942-245-97	Sequence 97, Appl
702	21	21.2	12	4	US-09-027-108C-5	Sequence 5, Appl1	775	21	21.2	16	1	US-07-942-245-99	Sequence 99, Appl
703	21	21.2	12	4	US-09-638-202A-118	Sequence 118, App	776	21	21.2	16	1	US-07-942-245-102	Sequence 102, App
704	21	21.2	12	5	PCT-US95-05471-55	Sequence 55, Appl	777	21	21.2	16	1	US-07-942-245-118	Sequence 118, App
705	21	21.2	12	5	PCT-US96-09809-155	Sequence 155, App	778	21	21.2	16	1	US-07-942-245-122	Sequence 122, App
706	21	21.2	12	6	5210075-52	Patent No. 5210075	779	21	21.2	16	1	US-07-942-245-146	Sequence 146, App
707	21	21.2	13	1	US-08-469-582-2	Sequence 2, Appl1	780	21	21.2	16	1	US-07-788-912-5	Sequence 175, App
708	21	21.2	13	1	US-08-469-582-18	Sequence 18, Appl	781	21	21.2	16	1	US-08-077-797A-1	Sequence 5, Appl1
709	21	21.2	13	4	US-08-946-525-8	Sequence 8, Appl1	782	21	21.2	16	1	US-08-474-587-3	Sequence 3, Appl1
710	21	21.2	13	4	US-08-392-542-5	Sequence 5, Appl1	783	21	21.2	16	2	US-08-337-646A-16	Sequence 16, Appl
711	21	21.2	13	4	US-09-206-059-12	Sequence 12, Appl	784	21	21.2	16	2	US-08-368-834-8	Sequence 8, Appl
712	21	21.2	13	4	US-09-177-249-34	Sequence 34, Appl	785	21	21.2	16	3	US-08-447-154-8	Sequence 8, Appl1
713	21	21.2	13	4	US-08-894-327-5	Sequence 5, Appl1	786	21	21.2	16	3	US-08-556-965-19	Sequence 19, Appl
714	21	21.2	13	4	US-09-261-855-6	Sequence 6, Appl1	787	21	21.2	16	3	US-08-556-965-25	Sequence 25, Appl
715	21	21.2	13	4	US-08-687-590-68	Sequence 68, Appl	788	21	21.2	16	3	US-08-604-965E-5	Sequence 5, Appl1
716	21	21.2	13	4	US-09-685-027-5	Sequence 5, Appl1	789	21	21.2	16	4	US-08-736-915-5	Sequence 5, Appl1
717	21	21.2	13	4	US-09-599-286-8	Sequence 8, Appl1	790	21	21.2	16	4	US-08-927-326-16	Sequence 16, Appl
718	21	21.2	13	5	PCT-US94-10257A-50	Sequence 50, Appl	791	21	21.2	16	4	US-08-602-999A-169	Sequence 169, App
719	21	21.2	14	1	US-08-164-618-12	Sequence 12, Appl	792	21	21.2	16	5	US-09-500-124-169	Sequence 1, Appl1
720	21	21.2	14	1	US-08-164-618-13	Sequence 13, Appl	793	21	21.2	16	5	PCT-US94-01238-1	Sequence 1, Appl1
721	21	21.2	14	1	US-08-164-618-14	Sequence 14, Appl	794	21	21.2	17	1	5278286-4	Sequence 7, Appl1
722	21	21.2	14	1	US-08-164-618-15	Sequence 15, Appl	795	21	21.2	17	1	US-08-066-239-7	Sequence 7, Appl1
723	21	21.2	14	1	US-08-164-618-19	Sequence 19, Appl	796	21	21.2	17	2	US-08-265-047-11	Sequence 11, Appl
724	21	21.2	14	1	US-07-694-469A-20	Sequence 20, Appl	797	21	21.2	17	2	US-08-424-268-4	Sequence 4, Appl1
725	21	21.2	14	1	US-08-111-080-6	Sequence 6, Appl1	798	21	21.2	17	2	US-08-824-151-2	Sequence 1, Appl1
726	21	21.2	14	1	US-08-258-851-7	Sequence 7, Appl1	799	21	21.2	17	2	US-08-824-151-1	Sequence 2, Appl1
727	21	21.2	14	1	US-08-211-980-6	Sequence 6, Appl1	800	21	21.2	17	2	US-08-621-803-6	Sequence 6, Appl1
728	21	21.2	14	1	US-08-321-668-21	Sequence 21, Appl	801	21	21.2	17	2	US-08-429-964-68	Sequence 68, Appl
729	21	21.2	14	1	US-08-321-668-25	Sequence 25, Appl	802	21	21.2	17	2	US-09-115-209-8	Sequence 8, Appl1
730	21	21.2	14	1	US-08-321-668-40	Sequence 40, Appl	803	21	21.2	17	4	US-09-217-352-6	Sequence 6, Appl1
731	21	21.2	14	1	US-08-321-668-41	Sequence 41, Appl	804	21	21.2	17	4	US-08-918-428D-15	Sequence 15, Appl
732	21	21.2	14	1	US-08-321-668-42	Sequence 42, Appl	805	21	21.2	17	5	US-09-265-653-20	Sequence 20, Appl
733	21	21.2	14	1	US-08-837-941-21	Sequence 21, Appl	806	21	21.2	17	5	PCT-US93-08062-68	Sequence 68, Appl
734	21	21.2	14	1	US-08-837-941-25	Sequence 25, Appl	807	21	21.2	17	5	PCT-US93-10442-4	Sequence 4, Appl1
735	21	21.2	14	1	US-08-837-941-40	Sequence 40, Appl	808	21	21.2	18	1	5219837-8	Sequence 15, Appl1
736	21	21.2	14	1	US-08-837-941-41	Sequence 41, Appl	809	21	21.2	18	2	US-08-325-243A-15	Sequence 15, Appl
737	21	21.2	14	1	US-08-837-941-42	Sequence 42, Appl	810	21	21.2	18	2	US-07-876-941A-29	Sequence 29, Appl
738	21	21.2	14	1	US-08-476-405A-24	Sequence 24, Appl	811	21	21.2	18	2	US-08-649-991-48	Sequence 48, Appl
739	21	21.2	14	4	US-08-448-489-8	Sequence 29, Appl	812	21	21.2	18	2	US-08-649-991-55	Sequence 55, Appl
740	21	21.2	14	4	US-08-448-489-22	Sequence 8, Appl1	813	21	21.2	18	2	US-09-017-205-61	Sequence 61, Appl
741	21	21.2	14	4	US-08-895-590-22	Sequence 22, Appl	814	21	21.2	18	2	US-09-017-205-66	Sequence 66, Appl
742	21	21.2	14	4	US-08-895-590-22	Sequence 40, Appl	815	21	21.2	18	2	US-08-476-866-8	Sequence 8, Appl1
743	21	21.2	14	5	PCT-US81-08328-36	Sequence 36, Appl	816	21	21.2	18	4	US-08-476-866-8	Sequence 6, Appl1
744	21	21.2	14	5	PCT-US92-07111-6	Sequence 6, Appl1	817	21	21.2	18	4	US-08-604-365-31	Sequence 31, Appl
745	21	21.2	14	5	PCT-US93-06751-90	Sequence 90, Appl	818	21	21.2	18	4	US-08-895-590-28	Sequence 28, Appl
746	21	21.2	14	5	PCT-US93-07967-6	Sequence 6, Appl1	819	21	21.2	18	4	US-09-142-680-23	Sequence 23, Appl
747	21	21.2	15	1	US-07-859-291C-5	Sequence 5, Appl1	820	21	21.2	18	5	PCT-US92-07865-8	Sequence 8, Appl1
748	21	21.2	15	1	US-07-859-291C-10	Sequence 10, Appl	821	21	21.2	18	6	5187077-36	Sequence 36, Appl
749	21	21.2	15	1	US-08-221-583-23	Sequence 23, Appl	822	21	21.2	19	1	US-08-634-060-42	Sequence 42, Appl
750	21	21.2	15	1	US-08-218-025A-185	Sequence 185, App	823	21	21.2	19	3	US-08-448-194-37	Sequence 37, Appl
751	21	21.2	15	1	US-08-208-181A-18	Sequence 18, Appl	824	21	21.2	19	4	US-08-867-921-37	Sequence 92, Appl
752	21	21.2	15	1	US-08-095-332-8	Sequence 8, Appl1	825	21	21.2	19	4	US-09-441-502B-62	Sequence 62, Appl
753	21	21.2	15	1	US-08-625-691-2	Sequence 2, Appl1	826	21	21.2	20	1	US-08-399-646-9	Sequence 9, Appl1
754	21	21.2	15	2	US-07-760-530-8	Sequence 8, Appl1	827	21	21.2	20	1	US-08-111-080-9	Sequence 9, Appl1
755	21	21.2	15	2	US-08-454-267-3	Sequence 3, Appl1	828	21	21.2	20	1	US-07-951-715A-75	Sequence 75, Appl
756	21	21.2	15	2	US-08-583-569-2	Sequence 2, Appl1	829	21	21.2	20	1	US-08-208-181A-3	Sequence 3, Appl1
757	21	21.2	15	2	US-08-941-319-3	Sequence 3, Appl1	830	21	21.2	20	1	US-08-211-980-9	Sequence 9, Appl1



831	21	21.2	20	1	US-08-607-321-9	Sequence 9, App11	904	21	21.2	23	3	US-08-646-273-1	Sequence 1, App11
832	21	21.2	20	2	US-08-961-240-9	Sequence 9, App11	905	21	21.2	23	4	US-08-736-151-7	Sequence 7, App11
833	21	21.2	20	2	US-08-605-501-9	Sequence 9, App11	906	21	21.2	23	4	US-09-150-1608-12	Sequence 12, App1
834	21	21.2	20	2	US-08-337-646A-27	Sequence 27, App1	907	21	21.2	23	4	US-08-734-607B-16	Sequence 6, App11
835	21	21.2	20	2	US-08-459-448A-75	Sequence 75, App1	908	21	21.2	23	4	US-09-230-548-14	Sequence 14, App1
836	21	21.2	20	2	US-08-581B-24	Sequence 24, App1	909	21	21.2	23	4	US-09-028-837-11	Sequence 11, App1
837	21	21.2	20	3	US-08-459-595A-75	Sequence 75, App1	910	21	21.2	23	5	PCT-US92-07111-10	Sequence 10, App1
838	21	21.2	20	3	US-08-872-094-13	Sequence 13, App1	911	21	21.2	23	5	PCT-US93-07967-10	Sequence 10, App1
839	21	21.2	20	3	US-08-459-504B-75	Sequence 75, App1	912	21	21.2	24	3	US-08-146-028-72	Sequence 72, App1
840	21	21.2	20	3	US-08-513-968-64	Sequence 64, App1	913	21	21.2	24	3	US-08-467-023-193	Sequence 193, App
841	21	21.2	20	3	US-08-459-444-75	Sequence 75, App1	914	21	21.2	24	4	US-08-855-958-6	Sequence 6, App11
842	21	21.2	20	4	US-08-612-973-66	Sequence 66, App1	915	21	21.2	24	4	US-08-723-425A-72	Sequence 72, App1
843	21	21.2	20	4	US-08-392-542-8	Sequence 8, App11	916	21	21.2	24	4	US-08-392-542-10	Sequence 10, App1
844	21	21.2	20	4	US-08-392-542-9	Sequence 9, App11	917	21	21.2	24	4	US-09-112-006-12	Sequence 12, App1
845	21	21.2	20	4	US-08-505-250-23	Sequence 23, App1	918	21	21.2	24	4	US-09-098-901-6	Sequence 6, App11
846	21	21.2	20	4	US-08-927-326-27	Sequence 27, App1	919	21	21.2	24	4	US-08-894-327-10	Sequence 10, App1
847	21	21.2	20	4	US-08-927-597-66	Sequence 66, App1	920	21	21.2	24	4	US-09-230-548-18	Sequence 18, App1
848	21	21.2	20	4	US-08-894-327-9	Sequence 9, App11	921	21	21.2	24	4	US-09-230-548-29	Sequence 29, App1
849	21	21.2	20	4	US-08-894-327-9	Sequence 9, App11	922	21	21.2	24	4	US-09-230-548-30	Sequence 30, App1
850	21	21.2	20	4	US-08-341-555-1	Sequence 1, App11	923	21	21.2	25	1	US-07-976-358-10	Sequence 10, App1
851	21	21.2	20	4	US-09-330-740A-1	Sequence 1, App11	924	21	21.2	25	1	US-07-976-358-10	Sequence 10, App1
852	21	21.2	20	4	US-09-547-422-75	Sequence 75, App1	925	21	21.2	25	1	US-08-209-525-32	Sequence 32, App1
853	21	21.2	20	4	US-08-505-250-23	Sequence 23, App1	926	21	21.2	25	1	US-08-362-567-2	Sequence 2, App11
854	21	21.2	20	4	US-09-304-711-24	Sequence 24, App1	927	21	21.2	25	2	US-08-677-298-3	Sequence 3, App11
855	21	21.2	20	4	US-09-685-027-8	Sequence 8, App11	928	21	21.2	25	3	US-08-846-444-7	Sequence 7, App11
856	21	21.2	20	4	US-09-685-027-9	Sequence 9, App11	929	21	21.2	25	4	US-08-392-542-11	Sequence 11, App1
857	21	21.2	20	4	US-09-643-597-242	Sequence 242, App	930	21	21.2	25	4	US-08-894-327-11	Sequence 11, App1
858	21	21.2	20	4	US-09-643-597-245	Sequence 245, App	931	21	21.2	25	4	US-08-909-531-8	Sequence 8, App11
859	21	21.2	20	4	US-09-643-597-246	Sequence 246, App	932	21	21.2	25	4	US-09-227-357-334	Sequence 334, App
860	21	21.2	20	4	US-09-643-597-367	Sequence 367, App	933	21	21.2	25	4	US-09-685-027-11	Sequence 11, App1
861	21	21.2	20	4	US-09-173-281-24	Sequence 24, App1	934	21	21.2	25	6	5178861-14	Patent No. 5178861
862	21	21.2	20	5	PCT-US92-07111-9	Sequence 9, App11	935	20.5	20.7	10	4	US-09-230-548-2	Sequence 2, App11
863	21	21.2	20	5	PCT-US93-07967-9	Sequence 9, App11	936	20.5	20.7	15	2	US-08-811-028-12	Sequence 12, App1
864	21	21.2	20	5	PCT-US94-10257A-78	Sequence 78, App1	937	20.5	20.7	15	2	PCT-US92-10068-16	Sequence 16, App1
865	21	21.2	20	5	PCT-US94-10257A-79	Sequence 79, App1	938	20.5	20.7	15	6	5187155-21	Patent No. 5187155
866	21	21.2	21	1	US-08-119-169A-1	Sequence 1, App11	939	20.5	20.7	17	2	US-09-115-209-47	Sequence 47, App1
867	21	21.2	21	1	US-08-279-906A-20	Sequence 20, App11	940	20.5	20.7	17	2	US-09-115-209-48	Sequence 48, App1
868	21	21.2	21	1	US-08-053-131-85	Sequence 85, App1	941	20.5	20.7	18	4	US-08-535-661-17	Sequence 17, App1
869	21	21.2	21	1	US-08-645-641-85	Sequence 85, App1	942	20.5	20.7	19	4	US-08-535-661-18	Sequence 18, App1
870	21	21.2	21	1	US-08-476-405A-13	Sequence 13, App1	943	20.5	20.7	20	1	US-07-718-274A-7	Sequence 7, App11
871	21	21.2	21	1	US-07-853-408B-85	Sequence 85, App1	944	20.5	20.7	20	1	US-07-718-274A-12	Sequence 12, App1
872	21	21.2	21	2	US-08-096-762-85	Sequence 85, App1	945	20.5	20.7	20	1	US-07-718-274A-29	Sequence 29, App1
873	21	21.2	21	2	US-08-308-865-85	Sequence 85, App1	946	20.5	20.7	20	1	US-08-149-106-7	Sequence 7, App11
874	21	21.2	21	2	US-08-675-631-2	Sequence 2, App11	947	20.5	20.7	20	1	US-08-149-106-12	Sequence 12, App1
875	21	21.2	21	4	US-08-675-631-10	Sequence 10, App1	948	20.5	20.7	20	1	US-08-149-106-29	Sequence 29, App1
876	21	21.2	21	4	US-08-957-001B-23	Sequence 23, App1	949	20.5	20.7	20	1	US-08-298-021-7	Sequence 7, App11
877	21	21.2	21	4	US-09-496-301-23	Sequence 23, App1	950	20.5	20.7	20	1	US-08-298-021-12	Sequence 12, App1
878	21	21.2	21	4	US-09-042-353-282	Sequence 282, App	951	20.5	20.7	20	1	US-08-298-021-29	Sequence 29, App1
879	21	21.2	21	4	US-09-612-126-3	Sequence 3, App11	952	20.5	20.7	20	4	US-08-535-661-19	Sequence 19, App1
880	21	21.2	21	4	US-08-756-417A-130	Sequence 130, App	953	20.5	20.7	20	4	US-09-064-411A-48	Sequence 48, App1
881	21	21.2	21	4	US-09-286-959B-21	Sequence 21, App1	954	20.5	20.7	21	4	US-08-535-661-20	Sequence 20, App1
882	21	21.2	21	5	US-09-508-803-3	Sequence 3, App11	955	20.5	20.7	22	1	US-07-698-928A-1	Sequence 1, App11
883	21	21.2	21	5	PCT-US92-10983-85	Sequence 85, App1	956	20.5	20.7	22	4	US-08-535-661-21	Sequence 21, App1
884	21	21.2	22	1	US-07-933-469A-7	Sequence 7, App11	957	20.5	20.7	23	4	US-08-535-661-22	Sequence 22, App1
885	21	21.2	22	1	US-08-250-310-7	Sequence 7, App11	958	20.5	20.7	24	1	US-07-698-928A-8	Sequence 8, App11
886	21	21.2	22	1	US-08-439-404-7	Sequence 7, App11	959	20.5	20.7	24	3	US-08-782-9977A-35	Sequence 35, App1
887	21	21.2	22	1	US-08-321-658-6	Sequence 6, App11	960	20.5	20.7	24	4	US-08-535-661-23	Sequence 23, App1
888	21	21.2	22	1	US-08-837-941-6	Sequence 6, App11	961	20.5	20.7	25	4	US-08-535-661-24	Sequence 24, App1
889	21	21.2	22	1	US-08-484-635-134	Sequence 134, App	962	20.5	20.7	5	1	US-08-406-132-42	Sequence 42, App1
890	21	21.2	22	2	US-08-484-631-134	Sequence 134, App	963	20.5	20.7	5	1	US-08-545-151-42	Sequence 42, App1
891	21	21.2	22	2	US-08-143-311B-1	Sequence 1, App11	964	20.5	20.7	6	1	US-08-169-743-2	Sequence 2, App11
892	21	21.2	22	2	US-08-345-321-19	Sequence 19, App1	965	20.5	20.7	6	1	US-08-178-482-7	Sequence 7, App11
893	21	21.2	22	2	US-08-345-321-21	Sequence 21, App1	966	20.5	20.7	6	1	US-08-234-997-1	Sequence 1, App11
894	21	21.2	22	2	US-08-827-570-134	Sequence 134, App	967	20.5	20.7	6	2	US-08-733-505A-5	Sequence 5, App11
895	21	21.2	22	3	US-08-839-327-7	Sequence 7, App11	968	20.5	20.7	6	2	US-08-345-321-13	Sequence 13, App1
896	21	21.2	22	3	US-09-340-781B-7	Sequence 7, App11	969	20.5	20.7	6	2	US-08-535-400-21	Sequence 21, App1
897	21	21.2	22	4	US-08-753-851-1	Sequence 1, App11	970	20.5	20.7	6	2	US-08-747-137-74	Sequence 74, App1
898	21	21.2	22	5	PCT-US92-08094-5	Sequence 5, App11	971	20.5	20.7	6	3	US-08-747-137-176	Sequence 176, App
899	21	21.2	23	1	US-08-111-080-10	Sequence 10, App1	972	20.5	20.7	6	3	US-08-956-639-1	Sequence 1, App11
900	21	21.2	23	1	US-08-211-980-10	Sequence 10, App1	973	20.5	20.7	6	4	US-09-020-880-50	Sequence 50, App1
901	21	21.2	23	1	US-08-487-001A-29	Sequence 29, App1	974	20.5	20.7	6	4	US-09-020-880-60	Sequence 60, App1
902	21	21.2	23	2	US-08-630-822A-29	Sequence 29, App1	975	20.5	20.7	6	4	US-09-178-115-103	Sequence 103, App
903	21	21.2	23	2	US-09-005-069-29	Sequence 29, App1	976	20.5	20.7	6	4	US-09-177-776-103	Sequence 103, App

777 20 20.2 6 4 US-09-101-544-52 Sequence 52, Appl  
 978 20 20.2 6 4 US-09-101-544-60 Sequence 60, Appl  
 979 20 20.2 6 4 US-09-606-477-1 Sequence 1, Appl  
 980 20 20.2 6 5 PCT-US93-05640-45 Sequence 45, Appl  
 981 20 20.2 7 1 US-08-421-702A-12 Sequence 12, Appl  
 982 20 20.2 7 1 US-08-303-052A-12 Sequence 12, Appl  
 983 20 20.2 7 1 US-08-421-696A-12 Sequence 12, Appl  
 984 20 20.2 7 1 US-08-421-697A-12 Sequence 12, Appl  
 985 20 20.2 7 1 US-08-421-698A-12 Sequence 12, Appl  
 986 20 20.2 7 2 US-08-421-695A-12 Sequence 12, Appl  
 987 20 20.2 7 5 PCT-US95-04741-12 Sequence 12, Appl  
 988 20 20.2 8 1 US-08-468-674B-83 Sequence 83, Appl  
 989 20 20.2 8 1 US-08-403-634-9 Sequence 9, Appl  
 990 20 20.2 8 1 US-08-403-634-13 Sequence 13, Appl  
 991 20 20.2 8 1 US-08-780-571-83 Sequence 83, Appl  
 992 20 20.2 8 2 US-08-747-137-75 Sequence 75, Appl  
 993 20 20.2 8 3 US-08-785-247-26 Sequence 26, Appl  
 994 20 20.2 8 4 US-08-913-441B-9 Sequence 9, Appl  
 995 20 20.2 8 4 US-08-913-441B-13 Sequence 13, Appl  
 996 20 20.2 8 4 US-09-108-857-7 Sequence 7, Appl  
 997 20 20.2 9 1 US-08-445-745-114 Sequence 114, App  
 998 20 20.2 9 2 US-08-101-624-17 Sequence 17, Appl  
 999 20 20.2 9 2 US-08-986-234-40 Sequence 40, Appl  
 1000 20 20.2 9 3 US-08-159-339A-334 Sequence 334, App

## ALIGNMENTS

RESULT 1  
 US-08-726-306A-61  
 ; Sequence 61, Application US/08726306A

Patent No. 5958684

GENERAL INFORMATION:

APPLICANT: van Leeuwen, Frederik Willem

APPLICANT: Burbach, Johannes Peter Henri

APPLICANT: Grosveld, Franklin G.

TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS

NUMBER OF SEQUENCES: 189

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: 1 Financial Center

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,306A

FILING DATE: 02-Oct-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 95/20080.4

FILING DATE: 02-Oct-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/009,832

FILING DATE: 01-Jan-1996

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Ph.D., Kathleen M.

REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9100

TELEFAX: (617) 345-9111

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-726-306A-61

Query Match

Best Local Similarity 100.0%; Score 99; DB 2; Length 25;

Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NVPGERMGRGRTSSKELA 19

Db 7 NVPGERMGRGRTSSKELA 25

RESULT 2  
 US-08-726-306A-87  
 ; Sequence 87, Application US/08726306A

Patent No. 5958684

GENERAL INFORMATION:

APPLICANT: van Leeuwen, Frederik Willem

APPLICANT: Burbach, Johannes Peter Henri

APPLICANT: Grosveld, Franklin G.

TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS

NUMBER OF SEQUENCES: 189

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: 1 Financial Center

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,306A

FILING DATE: 02-Oct-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 95/20080.4

FILING DATE: 02-Oct-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/009,832

FILING DATE: 01-Jan-1996

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Ph.D., Kathleen M.

REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9100

TELEFAX: (617) 345-9111

INFORMATION FOR SEQ ID NO: 87:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-726-306A-87

Query Match 100.0%; Score 99; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 4e-11;

Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NVPGERMGRGRTSSKELA 19

Db 7 NVPGERMGRGRTSSKELA 25

RESULT 3

US-08-726-306A-1

; Sequence 1, Application US/08726306A

; Patent No. 5958684

; GENERAL INFORMATION:

APPLICANT: van Leeuwen, Frederik Willem  
APPLICANT: Burbach, Johannes Peter Henri  
APPLICANT: Grosveld, Franklin G.  
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS  
NUMBER OF SEQUENCES: 189  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Banner & Wilcoff, Ltd.  
STREET: 1 Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,306A  
FILING DATE: 02-Oct-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 95/20080.4  
FILING DATE: 02-Oct-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/009,832  
FILING DATE: 01-Jan-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 345-9100  
TELEFAX: (617) 345-9111  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-726-306A-1

Query Match 47.5%; Score 47; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RGRSSKELA 19  
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Db 1 RGRSSKELA 10

RESULT 4  
US-09-540-224-9  
Sequence 9, Application US/09540224  
Patent No. 6468543  
GENERAL INFORMATION:  
APPLICANT: Gilbertson, Debra G.  
APPLICANT: Hart, Charles E.  
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4  
FILE REFERENCE: 00-28  
CURRENT APPLICATION NUMBER: US/09/540,224  
CURRENT FILING DATE: 2000-03-31  
EARLIER APPLICATION NUMBER: US 60/180,169  
EARLIER FILING DATE: 2000-02-04  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 24  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: peptide

US-09-540-224-9

Query Match 33.8%; Score 33.5; DB 4; Length 24;  
Best Local Similarity 58.3%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 3 PGRHMRGRRTSS 13  
|||  
Db 4 PGRHMRGRRTSS 15

RESULT 5  
US-08-077-797A-34  
Sequence 34, Application US/08077797A  
Patent No. 5679548  
GENERAL INFORMATION:  
APPLICANT: Barbas, Carlos F.  
APPLICANT: Rosenblum, Jonathan  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL  
TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5679548th Torrey Pines Road, TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/077,797A  
FILING DATE: 14-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,566  
FILING DATE: 02-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRL276P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
FRAGMENT TYPE: Internal  
US-08-077-797A-34

Query Match 32.3%; Score 32; DB 1; Length 16;  
Best Local Similarity 38.5%; Pred. No. 21;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGRHMRGRRTSS 15  
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Db 4 PGRHMRGRRTSS 16

RESULT 6  
PCT-US94-01238-34  
Sequence 34, Application PC/TUS9401238  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL

TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF  
NUMBER OF SEQUENCES: 65  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01238  
FILING DATE: 01-FEB-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/077,797  
FILING DATE: 14-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,566  
FILING DATE: 02-FEB-1993  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
PCT-US94-01238-34

Query Match 32.3%; Score 32; DB 5; Length 16;  
Best Local Similarity 38.5%; Pred. No. 21;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGRHMGGRGRTSS 15  
DB 4 PGRHMGGRGRTSS 16

RESULT 7  
US-07-841-591A-11  
Sequence 11, Application US/07841591A  
Patent No. 5900476  
GENERAL INFORMATION:  
APPLICANT: Ruggeri, Zaverio M. and  
APPLICANT: Ware, Jerry, inventors  
APPLICANT: on behalf of The Scripps Research  
TITLE OF INVENTION: Therapeutic Domains of  
TITLE OF INVENTION: von Willebrand Factor  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute  
STREET: 10666 No. 5900476th Torrey Pines Road  
CITY: La Jolla  
STATE: California  
COUNTRY: United States  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.2 megabyte 5 1/4" floppy  
COMPUTER: AST Bravo 386SX  
OPERATING SYSTEM: MS DOS version 3.2  
SOFTWARE: Wordperfect 5.1 conv. to ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/841,591A  
FILING DATE: 26-FEB-92  
CLASSIFICATION:  
PRIOR APPLICATION DATA: This is a c-i-p of  
APPLICATION NUMBER: PCT/US91/07756  
FILING DATE: 17-Oct-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Barron, Alexis  
REGISTRATION NUMBER: 22,702  
REFERENCE/DOCKET NUMBER: P16,633-H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 923-4466  
TELEFAX: (215) 923-2189  
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 21  
TYPE: Amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-07-841-591A-11

Query Match 32.3%; Score 32; DB 2; Length 21;  
Best Local Similarity 35.3%; Pred. No. 28;  
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 NVPGRHMGGRGRTSSKE 17  
DB 3 SMTGGQGMGRGSPGLQE 19

RESULT 8  
PCT-US93-02034-11  
Sequence 11, Application PC/TUS9302034  
GENERAL INFORMATION:  
APPLICANT: Ruggeri, Zaverio M. and  
APPLICANT: Ware, Jerry, inventors  
APPLICANT: on behalf of The Scripps Research  
TITLE OF INVENTION: Therapeutic Domains of  
TITLE OF INVENTION: von Willebrand Factor  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute  
STREET: 10666 North Torrey Pines Road  
CITY: La Jolla  
STATE: California  
COUNTRY: United States  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 2 megabyte 3.25" floppy  
COMPUTER: AST Bravo 386SX  
OPERATING SYSTEM: MS DOS version 3.2  
SOFTWARE: Wordperfect 5.1 conv. to ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02034  
FILING DATE: 19930223  
CLASSIFICATION:  
PRIOR APPLICATION DATA: This is a c-i-p of  
APPLICATION NUMBER: PCT/US91/07756  
FILING DATE: 17-Oct-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Barron, Alexis  
REGISTRATION NUMBER: 22,702  
REFERENCE/DOCKET NUMBER: P16,633-H PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 923-4466  
TELEFAX: (215) 923-2189  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: Linear  
PCT-US93-02034-11

Query Match 32.3%; Score 32; DB 5; Length 21;  
Best Local Similarity 35.3%; Pred. No. 28;  
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 NVPGRHMGGRGRTSSKE 17  
DB 3 SMTGGQGMGRGSPGLQE 19

RESULT 9  
US-09-047-026A-9  
Sequence 9, Application US/09047026A

```

1 OPERATING SYSTEM: PC-DOS/MS-DOS
2 SOFTWARE: PatentIn Release #1.0, Version #1.25
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: PCT/US93/06751
5 FILING DATE: 19930719
6 CLASSIFICATION:
7 ATTORNEY/AGENT INFORMATION:
8 NAME: Meredith, Roy D.
9 REGISTRATION NUMBER: 30,777
10 REFERENCE/DOCKET NUMBER: 18614
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: (908) 594-4678
13 TELEFAX: (908) 594-4720
14 TELEX: 138825
15 INFORMATION FOR SEQ ID NO: 106:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 14 amino acids
18 TYPE: amino acid
19 STRANDEDNESS: single
20 TOPOLOGY: linear
21 MOLECULE TYPE: peptide
22 HYPOTHEetical: NO
23 ANTI-SENSE: NO
24 IMMEDIATE SOURCE: Random Epitope Library Delta
25 PCT-US93-06751-106
26
27 Query Match 31.3%; Score 31; DB 5; Length 14;
28 Best Local Similarity 46.2%; Pred. No. 26;
29 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
30
31 QY 4 GHERMGRGRTSSK 16
32 |::|1111:1
33 Db 1 GVVKLGPGRTAGK 13
34
35 RESULT 11
36 US-07-942-245-142
37 Sequence 142 Application US/07942245
38 Patent No. 3639641
39 GENERAL INFORMATION:
40 APPLICANT: PEDERSEN, Jan T.
41 APPLICANT: SEARLE, Stephen M. J.
42 APPLICANT: REES, Anthony R.
43 APPLICANT: ROGUSKA, Michael A.
44 APPLICANT: GUILD, Braydon C.
45 TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
46 NUMBER OF SEQUENCES: 522
47 CORRESPONDENCE ADDRESS:
48 ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
49 STREET: 2100 Pennsylvania Avenue, N.W.
50 CITY: Washington
51 STATE: D.C.
52 COUNTRY: United States
53 ZIP: 20037-3202
54 COMPUTER READABLE FORM:
55 MEDIUM TYPE: floppy disk
56 COMPUTER: HP 9000/700 Workstation
57 OPERATING SYSTEM: UNIX
58 SOFTWARE: in house
59 CURRENT APPLICATION DATA:
60 APPLICATION NUMBER: US/07/942,245
61 FILING DATE: 09-SEP-1992
62 CLASSIFICATION: 530
63 TELECOMMUNICATION INFORMATION:
64 TELEPHONE: (202) 293-7060
65 TELEFAX: (202) 293-7860
66 TELEX: 6491103
67 INFORMATION FOR SEQ ID NO: 142:
68 SEQUENCE CHARACTERISTICS:
69 LENGTH: 16 amino acids
70 TYPE: amino acid
71 TOPOLOGY: linear
72

```

; MOLECULE TYPE: peptide  
US-07-942-245-142

Query Match 31.3%; Score 31; DB 1; Length 16;  
Best Local Similarity 58.3%; Pred. No. 31;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 RMGRGRTSSKEL 18  
| | | | | | | | | | | | | | | | | |  
DB 5 RPRGRRSSEKL 16

RESULT 12

US-09-166-028-3  
; Sequence 3, Application US/09166028  
; Patent No. 6245885  
; GENERAL INFORMATION:  
; APPLICANT: Gordon C. Shore et al.  
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING  
; FILE REFERENCE: 50013/011001  
; CURRENT APPLICATION NUMBER: US/09/166,028  
; CURRENT FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-166-028-3

Query Match 31.3%; Score 31; DB 4; Length 20;  
Best Local Similarity 40.0%; Pred. No. 40;  
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 GHERMGRRTSSKEL 18  
| | | | | | | | | | | | | | | | | |  
DB 5 GEPGRGGGPTSSKEL 19

RESULT 13  
US-08-874-569B-14  
; Sequence 14, Application US/08874569B  
; Patent No. 6306650  
; GENERAL INFORMATION:  
; APPLICANT: Townes, Tim M.  
; APPLICANT: Donze, David  
; TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND  
; FILE REFERENCE: 05118.000802  
; CURRENT APPLICATION NUMBER: US/08/874,569B  
; CURRENT FILING DATE: 1997-06-13  
; PRIOR APPLICATION NUMBER: 60/019,769  
; PRIOR FILING DATE: 1996-06-14  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: \ No. 6306650e =  
; OTHER INFORMATION: synthetic construct  
US-08-874-569B-14

Query Match 31.3%; Score 31; DB 4; Length 23;  
Best Local Similarity 40.0%; Pred. No. 47;  
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 GHERMGRRTSSKEL 18  
| | | | | | | | | | | | | | | | | |  
DB 2 GHGCGKSKSSSHL 16

RESULT 14

US-09-047-026A-15  
; Sequence 15, Application US/09047026A  
; Patent No. 5989897  
; GENERAL INFORMATION:  
; APPLICANT: Pillus, Lorraine  
; APPLICANT: Clarke, Astrid  
; APPLICANT: Lowell, Joana  
; APPLICANT: Jacobson, Sandra  
; APPLICANT: Reitsnyder, Cheryl  
; TITLE OF INVENTION: Yeast Silencing Genes, Proteins and  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/047,026A  
; FILING DATE: 24-MAR-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/042,375  
; FILING DATE: 24-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER: 1-97  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: YES  
US-09-047-026A-15

Query Match 31.3%; Score 31; DB 2; Length 24;  
Best Local Similarity 37.5%; Pred. No. 50;  
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 3 PGHERMGRRTSSKEL 18  
| | | | | | | | | | | | | | | | | |  
DB 8 PDYORGLGRALLEHL 23

RESULT 15

US-08-196-945-9  
; Sequence 9, Application US/08196945  
; Patent No. 5563032  
; GENERAL INFORMATION:  
; APPLICANT: FIELDS, HOWARD A.  
; APPLICANT: KHUDYAKOV, YURI E.  
; APPLICANT: FAVOROV, MICHAEL O.  
; TITLE OF INVENTION: MOSAIC POLYPEPTIDE AND METHODS FOR  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
; STREET: Suite 1200, The Candler Bldg.,

STREET: 127 Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/196,945  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spratt, Gwendolyn D.  
REGISTRATION NUMBER: 36,016  
REFERENCE/DOCKET NUMBER: 1414,099  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404/688-0770  
TELEFAX: 404/688-9880  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-196-945-9

Query Match 30.8%; Score 30.5; DB 1; Length 21;  
Best Local Similarity 45.0%; Pred. No. 52;  
Matches 9; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NVPGH-ERMGRGRTSKELA 19  
| | | | : | | | : | |  
Db 2 NOPGHLPAGEIRSPAPPLA 21

RESULT 16  
US-07-965-667A-10  
Sequence 10, Application US/07965667A  
Patent No. 5736315  
GENERAL INFORMATION:  
APPLICANT: Fields, Howard A.  
APPLICANT: Favorov, Michael O.  
APPLICANT: Khudyakov, Yuri E.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
TITLE OF INVENTION: ANTI-HEPATITIS E VIRUS ACTIVITY  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
STREET: 133 Carnegie Way, N.W., Suite 400  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,667A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spratt, Gwendolyn D.  
REGISTRATION NUMBER: 36,016  
REFERENCE/DOCKET NUMBER: 1414,022  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 688-0770  
TELEFAX: (404) 688-9880

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-965-667A-10

Query Match 30.8%; Score 30.5; DB 1; Length 21;  
Best Local Similarity 45.0%; Pred. No. 52;  
Matches 9; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NVPGH-ERMGRGRTSKELA 19  
| | | | : | | | : | |  
Db 2 NOPGHLPAGEIRSPAPPLA 21

RESULT 17  
US-08-484-819-10  
Sequence 10, Application US/08484819  
Patent No. 6022685  
GENERAL INFORMATION:  
APPLICANT: Fields, Howard A.  
APPLICANT: Favorov, Michael O.  
APPLICANT: Khudyakov, Yuri E.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
TITLE OF INVENTION: ANTI-HEPATITIS E VIRUS ACTIVITY  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
STREET: 133 Carnegie Way, N.W., Suite 400  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,819  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,667  
FILING DATE: 07-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Spratt, Gwendolyn D.  
REGISTRATION NUMBER: 36,016  
REFERENCE/DOCKET NUMBER: 1414,022  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 688-0770  
TELEFAX: (404) 688-9880  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-819-10

Query Match 30.8%; Score 30.5; DB 3; Length 21;  
Best Local Similarity 45.0%; Pred. No. 52;  
Matches 9; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NVPGH-ERMGRGRTSKELA 19  
| | | | : | | | : | |  
Db 2 NOPGHLPAGEIRSPAPPLA 21

RESULT 18  
PCT-US93-10197-10  
; Sequence 10, Application PC/TUS9310197  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: "METHODS AND COMPOSITIONS FOR DETECTING  
; TITLE OF INVENTION: ANTI-HEPATITIS E VIRUS ACTIVITY"  
; NUMBER OF SEQUENCES: 20  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25 EPO  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/10197  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/965,667  
; FILING DATE: 21-OCT-1992  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US93-10197-10

Query Match 30.8%; Score 30.5; DB 5; Length 21;  
Best Local Similarity 45.0%; Pred. No. 52;  
Matches 9; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 NVPGH-ERMGRGRTSSKELA 19  
Db 2 NPGHLAGLRPSAPPLA 21

RESULT 19  
US-08-651-818A-20  
; Sequence 20, Application US/08651818A  
; Patent No. 5948889  
; GENERAL INFORMATION:  
; APPLICANT: de Boer, Plet A.J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING  
; TITLE OF INVENTION: ANTIMICROBIALS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/651,818A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carroll, Peter G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: CASE-02249  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid

STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
US-08-651-818A-20

Query Match 30.3%; Score 30; DB 2; Length 14;  
Best Local Similarity 45.5%; Pred. No. 40;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 NVPGHERMGRG 11  
Db 3 SMTGGQGMGRG 13

RESULT 20  
US-08-722-806A-10  
; Sequence 10, Application US/08722806A  
; Patent No. 5981247  
; GENERAL INFORMATION:  
; APPLICANT: Hagedorn, Curt H.  
; TITLE OF INVENTION: Recombinant Hepatitis C Virus RNA  
; TITLE OF INVENTION: Replicase  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/722,806A  
; FILING DATE: 27-SEP-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/004383  
; FILING DATE: 27-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Greenlee, Lorraine L.  
; REGISTRATION NUMBER: 27,894  
; REFERENCE/DOCKET NUMBER: 76-950S  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-722-806A-10

Query Match 30.3%; Score 30; DB 2; Length 14;  
Best Local Similarity 45.5%; Pred. No. 40;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 NVPGHERMGRG 11  
Db 3 SMTGGQGMGRG 13

RESULT 21  
US-09-184-826-20  
; Sequence 20, Application US/09184826  
; Patent No. 6248543  
; GENERAL INFORMATION:  
; APPLICANT: de Boer, Plet A.J.



```

APPLICANT: Hale, Cynthia A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING
TITLE OF INVENTION: ANTIMICROBIALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: MEDLEN & CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,826
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: CASE-02249
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-184-826-20

Query Match      30.3%; Score 30; DB 4; Length 14;
Best Local Similarity 45.5%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 NVPGHERMGRG 11
Db 3 SMTGGQGMGRG 13

RESULT 22
US-09-337-028-10
; Sequence 10, Application US/09337028
; Patent No. 6248589
GENERAL INFORMATION:
APPLICANT: Hagedorn, Curt H.
APPLICANT: Al, Reinholdus H.
TITLE OF INVENTION: Recombinant Hepatitis C Virus RNA Replicase
FILE REFERENCE: RECOM HEPATITIS C VIRUS RNA REPLICASE
CURRENT APPLICATION NUMBER: US/09/337,028
CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: US 60/004,383
EARLIER FILING DATE: 1995-09-27
EARLIER APPLICATION NUMBER: US 08/722, 806
EARLIER FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-337-028-10

Query Match      30.3%; Score 30; DB 4; Length 14;
Best Local Similarity 45.5%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 NVPGHERMGRG 11
Db 3 SMTGGQGMGRG 13
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Db 3 SMTGGQGMGRG 13
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RESULT 23
US-09-597-877-10
; Sequence 10, Application US/09597877
; Patent No. 6461845
GENERAL INFORMATION:
APPLICANT: Hagedorn, Curt H.
TITLE OF INVENTION: Recombinant Hepatitis C Virus RNA Replicase
FILE REFERENCE: 76-95B
CURRENT APPLICATION NUMBER: US/09/597,877
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 60/004,383
PRIOR FILING DATE: 1995-09-27
PRIOR APPLICATION NUMBER: 08/722,806
PRIOR FILING DATE: 1996-09-27
PRIOR APPLICATION NUMBER: 09/337,028
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence of the cloning site in pET-11a where the
OTHER INFORMATION: 5' end of the PCR amplified NS5b gene was
US-09-597-877-10

Query Match      30.3%; Score 30; DB 4; Length 14;
Best Local Similarity 45.5%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 NVPGHERMGRG 11
Db 3 SMTGGQGMGRG 13

RESULT 24
US-08-310-912A-95
; Sequence 95, Application US/08310912A
; Patent No. 5981730
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,912A
FILING DATE: September 22, 1994
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CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/227,360  
FILING DATE: April 13, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lech, Karen F.  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/254001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 100254  
INFORMATION FOR SEQ ID NO: 95:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
08-310-912A-95

Query Match 29.3%; Score 29; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 40;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VPCHER 7  
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DB 3 VPGHTR 8

## RESULT 25

US-08-841-089-95  
Sequence 95, Application US/08841089  
Patent No. 6127607

## GENERAL INFORMATION:

APPLICANT: Ausubel, Frederick M.  
APPLICANT: Staskiewicz, Brian J.  
APPLICANT: Brent, Andrew F.  
APPLICANT: Dahlbeck, Douglas  
APPLICANT: Katagiri, Fumiaki  
APPLICANT: Kunkel, Barbara N.  
APPLICANT: Mindinos, Michael N.  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: RPS2 GENE AND USBS THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street Suite 3100  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2904

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/841,089  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,360  
FILING DATE: 13-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/230001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 100254  
INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-841-089-95

Query Match 29.3%; Score 29; DB 3; Length 10;  
Best Local Similarity 83.3%; Pred. No. 40;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VPCHER 7  
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DB 3 VPGHTR 8

Search completed: March 14, 2003, 16:07:34  
Job time : 38 secs

Nichols, C.  
091674913  
Seq. ID 1

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 16:02:37 ; Search time 36 Seconds  
(without alignments)  
70.327 Million cell updates/sec

Title: US-09-674-913A-1

Sequence: 1 NVPCHERMGRTSSKELA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 320064

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	100.0	19	AA556391	Mutant beta-APP pr
2	99	100.0	25	AA12019	Human beta-amyloid
3	82.5	83.3	19	AA59216	AM7 peptide. Uni
4	63	63.6	14	AA59215	AM7 peptide. Uni
5	58	58.6	12	AA56394	Mutant beta-APP pr
6	52.5	52.5	17	AA56393	Mutant beta-APP pr
7	47	47.5	10	AA18633	Peptide resulting
8	47	47.5	10	AA120152	Human beta-APP imm
9	47	47.5	10	AA59214	AM1 peptide. Uni
10	41	41.4	15	AA556395	Mutant ubiquitin-B

11	33.5	33.8	24	AA48661	Human zvegf4 pepti
12	33.5	33.8	24	AA65607	Human zvegf4 pepti
13	33.5	33.8	24	ABP51644	Human zvegf4 pepti
14	33.3	33.3	20	AB229938	Peptide #2589 enco
15	33.3	33.3	20	AB35121	Peptide #2627 enco
16	33.3	33.3	20	AA555944	Human brain expres
17	33.3	33.3	20	AA668310	Human bone marrow
18	33.3	33.3	20	AA603860	Peptide #2542 enco
19	33.3	33.3	20	AB37860	Human peptide enco
20	33.3	33.3	16	AA57938	Randomly generated
21	32.3	32.3	16	AA678090	Ce(III) metal ion
22	32.3	32.3	17	AA66845	Human gene 2 enco
23	32.3	32.3	16	AA678090	Human Immunodefici
24	32.3	32.3	18	AA604485	Human bone marrow
25	32.3	32.3	19	AA672540	Human peptide enco
26	32.3	32.3	21	AA642360	vWF-derived polype
27	32.3	32.3	21	AA638573	T7 derived fragmen
28	32.3	32.3	22	AA641274	SNP peptide 88.
29	32.3	32.3	25	AB62024	Human tumour suppr
30	32.3	32.3	14	AA47773	HIV epitope #106.
31	31.3	31.3	14	AA081823	Phosphinothricin a
32	31.3	31.3	16	AA52171	Human light chain
33	31.3	31.3	18	AA69144	Neuronal NOS bindi
34	31.3	31.3	20	AA590736	Human BAX amino ac
35	31.3	31.3	20	AA58365	Human brain expres
36	31.3	31.3	21	AA602873	Trypatic peptide #1
37	31.3	31.3	21	AA602826	Delta-EKLF polypep
38	31.3	31.3	21	AA602826	Hepatitis E virus
39	30.5	30.8	23	AA52590	HEV Mexico ORF3 ep
40	30.5	30.8	21	AA682205	Human glandular ka
41	30.5	30.8	16	AA682205	Human salivary PRP-1
42	30.3	30.3	8	AA648778	Arabidopsis thalia
43	30.3	30.3	9	AA648778	Human salivary PRP-1
44	30.3	30.3	10	AA648778	Human salivary PRP-1
45	30.3	30.3	14	AA65342	Seq ID No: 29 of W
46	30.3	30.3	14	AA65342	Human interleukin-
47	30.3	30.3	16	AA674943	Plasmod pET-3a pep
48	30.3	30.3	17	AA648783	Human salivary PRP-1
49	30.3	30.3	18	AA605540	Human salivary PRP-1
50	30.3	30.3	18	AA605540	Human salivary PRP-1
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53	30.3	30.3	19	AA645192	Human salivary PRP-1
54	30.3	30.3	20	AA645192	Human salivary PRP-1
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65	29.3	29.3	23	AA645192	Human salivary PRP-1
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69	29.3	29.3	24	AA645192	Human salivary PRP-1
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73	29.3	29.3	25	AA645192	Human salivary PRP-1
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79	29.3	29.3	25	AA645192	Human salivary PRP-1
80	29.3	29.3	25	AA645192	Human salivary PRP-1
81	29.3	29.3	25	AA645192	Human salivary PRP-1
82	29.3	29.3	25	AA645192	Human salivary PRP-1
83	29.3	29.3	25	AA645192	Human salivary PRP-1

84	28	28.3	14	22	AA65341	Human interleukin-1
85	28	28.3	15	18	AA30950	Timothy grass poll
86	28	28.3	15	20	AA22935	Peptide derived fr
87	28	28.3	15	20	AA22953	Synthetic peptide
88	28	28.3	16	15	AA52169	Human light chain
89	28	28.3	20	21	AA50993	Potato pr17-WT pro
90	28	28.3	20	22	AA80668	Human peptide #134
91	28	28.3	20	22	AA885140	Sequence of a synt
92	28	28.3	20	22	AA885141	Sequence of a synt
93	28	28.3	20	22	AA885142	Sequence of a synt
94	28	28.3	21	22	AA885143	Human dual-specific
95	28	28.3	22	20	AA22922	Flagrin derived a
96	28	28.3	22	20	AA22942	Synthetic peptide
97	28	28.3	22	20	AA22947	Synthetic peptide
98	28	28.3	23	23	AAE19024	Human ghrelin pept
99	28	28.3	24	22	AA891208	Insulin and insuli
100	28	28.3	25	22	AAV09077	EBP mutated fragm
101	28	28.3	25	22	ABG14181	Novel human diagno
102	27	27.3	8	18	AAW34356	PKB substrate #3.
103	27	27.3	8	21	AAV58257	Protein kinase B (
104	27	27.3	10	18	AAW15659	Platelet aggregati
105	27	27.3	10	22	AA694455	Human complementar
106	27	27.3	10	22	AA69174	Human complementar
107	27	27.3	10	22	AA685559	Saccharomyces cere
108	27	27.3	10	22	AA685565	Saccharomyces cere
109	27	27.3	10	22	AA685579	Saccharomyces cere
110	27	27.3	10	22	AA686075	Saccharomyces cere
111	27	27.3	10	22	ABP61350	Anti-thrombotic cy
112	27	27.3	11	17	AA698330	Interleukin-1 prod
113	27	27.3	11	18	AAW34354	PKB substrate #1.
114	27	27.3	11	21	AAV93506	Crosslink peptide
115	27	27.3	11	21	AAV93508	Peptide substrate
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117	27	27.3	11	21	AAV85173	Crosspeptide amino
118	27	27.3	11	21	AAV54015	Phosphoserine AKT
119	27	27.3	11	21	AAV58261	GSK3-derived pepti
120	27	27.3	11	21	AAV06068	Crosslink peptide
121	27	27.3	11	22	AA699789	Protein kinase B a
122	27	27.3	11	22	AAE04940	Nuclear Dbp2-relat
123	27	27.3	11	22	AAU02106	Human phosphorilat
124	27	27.3	11	22	AA697048	MSK substrate pept
125	27	27.3	11	22	AA697048	Crosslink peptide
126	27	27.3	12	22	AA698331	Interleukin-1 prod
127	27	27.3	12	23	AAU74498	Protein kinase B s
128	27	27.3	13	19	AA656812	Enzyme inhibitor p
129	27	27.3	13	23	ABG61650	Human G protein-co
130	27	27.3	14	22	AA698433	Human peptide #170
131	27	27.3	14	22	AAW05053	Human histone frag
132	27	27.3	15	15	AA647738	HIV epitope #71
133	27	27.3	15	20	AA40703	A3 derivative #24,
134	27	27.3	15	21	AA630042	Scatfold protein S
135	27	27.3	16	15	AA69507	Hydrophilic linker
136	27	27.3	16	15	AAU99157	Bovine chondroelek
137	27	27.3	16	23	AAE13272	Linker peptide to
138	27	27.3	17	20	AA685631	Antigenic epitope
139	27	27.3	18	23	AAE14576	Human JF463726 pep
140	27	27.3	20	15	AA675668	Human plasmin N-te
141	27	27.3	20	21	AA681350	Streptavidin displ
142	27	27.3	21	20	AA636587	Fragment of human
143	27	27.3	21	23	AB683068	M13 segment of smo
144	27	27.3	22	23	AA649321	HIV-1 gp120 V3 loo
145	27	27.3	22	23	AAE22752	Human dual-specific
146	27	27.3	23	22	ABG11033	Novel human diagno
147	27	27.3	24	14	AA641126	HCV peptide Xxb-1
148	27	27.3	25	20	AAV09074	EGBP mutated fragm
149	27	27.3	25	21	AAV52526	House dust mite al
150	27	27.3	25	22	AAU01686	Human secreted pro
151	27	27.3	25	23	AAU96350	Der HMW-map polype
152	26.5	26.8	16	19	AAW76431	PKB substrate 3-4 of
153	26	26.3	7	18	AAW34367	PKB substrate #14.
154	26	26.3	7	21	AAV9522	Peptide substrate
155	26	26.3	7	21	AAV95272	Crosslink-derived
156	26	26.3	7	23	ABG34942	Human bone marrow

Human complementar  
Human complementar  
Human complementar  
Human complementar  
Saccharomyces cere  
Saccharomyces cere  
Saccharomyces cere  
Human secreted pro  
Phosphorylated dhl  
HIV-2 strain ROD V  
Anti-methenyltetra  
Macrophage-colony  
Methenyltetrahydro  
Epstein-Barr virus  
Epstein-Barr virus  
Chenopodium album  
Fragment of pertus  
Human peptide #822  
Human peptide #823  
Human Interleukin-  
Human thyrocalcilo  
HER2/NEU DR superm  
Human protein phos  
Human leucocyte an  
Human light chain  
Human light chain  
Macaque histatin-1  
Macaque histatin 1  
Peptide #9360 enco  
Protein #7556 enco  
Human brain expres  
Human bone marrow  
Peptide #7065 enco  
Peptide #9690 enco  
Human peptide enco  
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Insulin/insulin-11  
Methylated Smb hom  
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Laminin A chain de  
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Peptide cfc3, base  
Macaque histatin 1  
BAX mutant peptide  
HIV-1 clinical str  
Bovine oncostatin  
Peptide sequence o  
Mouse BAX amino ac  
Rat BAX amino acid  
Human matrix metal  
OER antibody epito  
Feline FlAPp35 pro  
Novel human diagno  
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Peptide #1484 enco  
Protein #1415 enco  
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Human bone marrow  
Peptide #1432 enco  
Peptide #1471 enco  
Peptide #1407 enco  
Human peptide enco  
Macaque histatin-1  
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Peptide #2607 enco  
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HCV peptide xxd-1  
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Isolated peptide f  
Vitronectin fragme  
UPAR targeting seq

230	25.5	25.8	25	19	AAW60534	Sequence joint bet	303	25	25.3	15	22	ABP25386	HIV-1 epitope #40.
231	25.5	25.8	25	19	AAU933714	Dental product bon	304	25	25.3	15	22	ABP25388	HIV-1 epitope #42.
232	25.5	25.8	25	23	AAO20364	Peptide of matrix	305	25	25.3	15	23	ABP47084	Human Blys binding
233	25	25.3	25	22	AAAB0684	Human glandular ka	306	25	25.3	15	23	AAU78647	Synthetic peptide
234	25	25.3	25	13	AAAR7705	Peptide (205) inh1	307	25	25.3	15	23	AAE16617	Human KCNO5 immuno
235	25	25.3	25	17	AAW49339	Human leucocyte an	308	25	25.3	16	15	AAAR5217	Mouse light chain
236	25	25.3	25	9	AAW83400	Type II collagen m	309	25	25.3	16	16	AAAR70345	NE-AT transcriptio
237	25	25.3	25	21	AAAB19776	Protein tyrosine p	310	25	25.3	16	16	AAAR83275	HIV principal neut
238	25	25.3	25	9	AAE18745	Human leucocyte an	311	25	25.3	16	19	AAAB6359	Peptide MCL13 deri
239	25	25.3	25	23	AAU71305	Human MHC class I	312	25	25.3	16	21	AAAY6552	Human NF-ATc1 anti
240	25	25.3	25	9	AAU71395	Human MHC molecule	313	25	25.3	16	21	AAAY73152	Human NF-ATc1 anti
241	25	25.3	25	9	AAU71596	Human MHC class I	314	25	25.3	16	22	AAU12486	Human HIV-1 Th-CTL
242	25	25.3	25	23	AAU71698	Human MHC molecule	315	25	25.3	16	22	AAAB6484	Human NF-ATc1 pepid
243	25	25.3	25	9	AAU71736	Human MHC molecule	316	25	25.3	16	23	AAAE21546	Human NF-ATc1 anti
244	25	25.3	25	10	AAAR8329	Interleukin-1 prod	317	25	25.3	17	18	AAW67755	Thrombopoietin rec
245	25	25.3	25	10	AAAG95908	Human complementar	318	25	25.3	17	18	AAW09604	Thrombopoietin rec
246	25	25.3	25	10	AAAG83516	Arbidopsis thaila	319	25	25.3	17	20	AAAY6476	Fragment of human
247	25	25.3	25	10	AAAG84361	Arbidopsis thaila	320	25	25.3	17	22	AAAB28215	Human peptide #866
248	25	25.3	25	10	AAAG86859	Saccharomyces cere	321	25	25.3	17	22	ABAB33390	Peptide #896 encod
249	25	25.3	25	10	AAAG87824	Saccharomyces cere	322	25	25.3	17	22	ABAB18849	Protein #848 encod
250	25	25.3	25	10	AAAG87825	Saccharomyces cere	323	25	25.3	17	22	AAU25974	Human thrombopoiet
251	25	25.3	25	10	AAU71174	Human MHC class I	324	25	25.3	17	22	AAW54175	Human brain expres
252	25	25.3	25	10	AAU71268	Human MHC class I	325	25	25.3	17	22	AAAB6569	Human bone marrow
253	25	25.3	25	10	AAU71376	Human MHC class I	326	25	25.3	17	22	AAAM14442	Peptide #876 encod
254	25	25.3	25	10	AAU71452	Human MHC molecule	327	25	25.3	17	22	AAAM26855	Peptide #892 encod
255	25	25.3	25	10	AAU71571	Human MHC class I	328	25	25.3	17	22	AAAM02169	Peptide #851 encod
256	25	25.3	25	10	AAU71591	Human MHC class I	329	25	25.3	17	22	AAAB7996	L25 peptide derive
257	25	25.3	25	10	AAU71651	Human MHC class I	330	25	25.3	17	22	AAAB8157	Human MCH receptor
258	25	25.3	25	11	AAW09224	Repeat peptide use	331	25	25.3	17	23	ABG36221	Human peptide enco
259	25	25.3	25	11	AAAR8439	Peptide with cell	332	25	25.3	17	23	AAU10745	Human RGS18 N-term
260	25	25.3	25	11	AAW39794	Tobacco PABP repe	333	25	25.3	17	23	ABAB74819	Nuclear protein nu
261	25	25.3	25	11	AAW51894	Protocol X peptide	334	25	25.3	18	21	AAAB74251	M68 TNFR-like prot
262	25	25.3	25	11	AAW80341	Synthetic bioelast	335	25	25.3	18	22	AAAM60008	Human brain expres
263	25	25.3	25	11	AAW80343	Synthetic bioelast	336	25	25.3	18	22	AAAM72608	Human bone marrow
264	25	25.3	25	12	AAW07228	HIV-1 group O stra	337	25	25.3	18	23	AAAB8498	Insulin/insulin-1i
265	25	25.3	25	12	AAAR8441	Peptide with cell	338	25	25.3	19	19	AAAB1509	Peptide cfc5, base
266	25	25.3	25	12	AAW50247	T7-tag epitope. S	339	25	25.3	19	19	AAAB1514	Peptide cf, based
267	25	25.3	25	12	AAW8617	Peptide 30P used I	340	25	25.3	19	23	AAU80198	Human protein zero
268	25	25.3	25	13	AAW57036	Enzyme inhibitor P	341	25	25.3	20	17	AAAR8306	p21WAF1 peptide 6.
269	25	25.3	25	13	AAW56808	Enzyme inhibitor P	342	25	25.3	20	18	AAAM44229	Human p21waf1 frag
270	25	25.3	25	13	AAAB39635	Anti-IL12 antibody	343	25	25.3	20	21	AAAB13671	C. trachomatis OMC
271	25	25.3	25	13	AAAG73192	Protease binding s	344	25	25.3	20	21	AAAB13672	C. trachomatis OMC
272	25	25.3	25	13	AAAG73314	Protease indicator	345	25	25.3	20	21	AAAB18498	Peptide substrate
273	25	25.3	25	13	AAU98796	Bovine Ribosomal P	346	25	25.3	20	21	AAAY8349	Alpha D peptide de
274	25	25.3	25	13	ABP47170	Human Blys binding	347	25	25.3	20	22	AAAG83239	Chlamydia trachoma
275	25	25.3	25	14	AAAR8436	Peptide with cell	348	25	25.3	20	22	AAAG83240	Chlamydia trachoma
276	25	25.3	25	14	AAW86171	Peptide 30M used I	349	25	25.3	20	23	ABG62838	Ligand/receptor sp
277	25	25.3	25	14	AAW97536	Human peptide #811	350	25	25.3	20	23	ABG62839	DNA binding peptid
278	25	25.3	25	14	AAW88228	Human peptide #150	351	25	25.3	20	23	AAO17408	DNA binding peptid
279	25	25.3	25	14	AAW88685	Human peptide #196	352	25	25.3	20	23	AAO17416	Chlamydia peptide
280	25	25.3	25	14	AAU68487	Human Breast cance	353	25	25.3	20	23	ABAB4210	Chlamydia peptide
281	25	25.3	25	14	AAW00425	Human protein frag	354	25	25.3	20	23	ABAB4211	Chlamydia peptide
282	25	25.3	25	14	AAW00426	Human protein frag	355	25	25.3	21	19	AAAY21024	Human glial fibril
283	25	25.3	25	14	AAAG73313	Protease indicator	356	25	25.3	21	19	AAW46342	Amino acid sequenc
284	25	25.3	25	15	AAW85403	Helper T-cell clas	357	25	25.3	21	20	AAAY22147	Peptide used for F
285	25	25.3	25	15	AAW85340	Helper T-cell clas	358	25	25.3	21	21	AAAB37204	Repressifus-1 ICP2
286	25	25.3	25	15	AAW85205	Helper T-cell clas	359	25	25.3	21	22	AAAB35273	Human dual specifi
287	25	25.3	25	15	AAW85215	Helper T-cell pep	360	25	25.3	21	22	ABAB3070	Partial amino acid
288	25	25.3	25	15	AAW85205	PDZ3 specific pept	361	25	25.3	22	20	AAAY00773	Mouse tag7 clone p
289	25	25.3	25	15	AAW73153	HIV-derived MHC cl	362	25	25.3	22	21	AAAY98802	Human WT1 immunog
290	25	25.3	25	15	AAW73154	HIV-derived MHC cl	363	25	25.3	22	22	AAU68901	Human WT1 immunog
291	25	25.3	25	15	ABP24697	HIV DR super motif	364	25	25.3	22	22	AAAG62134	Human WT1 immunog
292	25	25.3	25	15	ABP24698	HIV DR super motif	365	25	25.3	22	23	ABG33371	C-terminus of myc-
293	25	25.3	25	15	ABP24743	HIV DR super motif	366	25	25.3	24	17	AAW07330	Human secreted pro
294	25	25.3	25	15	ABP24745	HIV DR super motif	367	25	25.3	24	21	AAAB51768	Human secreted pro
295	25	25.3	25	15	ABP25067	HIV DR supermotif	368	25	25.3	25	12	AAAR12282	Parvovirus B19 epi
296	25	25.3	25	15	ABP25068	HIV DR supermotif	369	25	25.3	25	15	AAAR47398	PDGF-activily-disp
297	25	25.3	25	15	ABP25255	HIV HLA-DR binding	370	25	25.3	25	20	AAAY09085	E6B8 mutated fragm
298	25	25.3	25	15	ABP25257	HIV HLA-DR binding	371	25	25.3	25	20	AAAY09086	E6B8 mutated fragm
299	25	25.3	25	15	ABP25274	HIV-derived DR-sup	372	25	25.3	25	20	AAAY09087	E6B8 mutated fragm
300	25	25.3	25	15	ABP25275	HIV-derived DR-sup	373	25	25.3	25	20	AAAY09088	E6B8 mutated fragm
301	25	25.3	25	15	ABP25332	HTL cadidate epito	374	25	25.3	25	20	AAAY09084	E6B8 mutated fragm
302	25	25.3	25	15	ABP25334	HTL cadidate epito	375	25	25.3	25	20	AAAY09082	E6B8 mutated fragm



522	24	24.2	18	21	AAV95915	Hypothetical signa	595	24	24.2	23	22	AAW03096	Peptide #1778 enco
523	24	24.2	18	21	AAV17119	Calmodulin antagon	596	24	24.2	23	23	AAW37119	Human peptide enco
524	24	24.2	18	22	AAW08086	DtxR homologue lig	597	24	24.2	24	18	AAW23495	Antibacterial and/
525	24	24.2	18	22	AAW61816	Ty59 polypeptide	598	24	24.2	24	19	AAW44187	Mateate cis-trans
526	24	24.2	18	22	AAW55529	Peptide linker #3.	599	24	24.2	24	20	AAW39412	Human interleukin-
527	24	24.2	18	22	AAW57786	Flexible polylinke	600	24	24.2	24	21	AAW18711	Synthetic peptide
528	24	24.2	18	22	AAW57786	Flexible polylinke	601	24	24.2	24	21	AAW18711	N-terminus of Haem
529	24	24.2	18	22	AAW73197	Catmodulin antagon	602	24	24.2	24	23	AAW17774	Human beta-defensi
530	24	24.2	19	14	AAW43042	N-terminal fragmen	603	24	24.2	24	23	AAW178012	Human interleukin
531	24	24.2	19	15	AAW58355	Porcine parvovirus	604	24	24.2	25	14	AAW41074	HYV-1 partial V3 1
532	24	24.2	19	19	AAW66629	HSV-2 glycoprotein	605	24	24.2	25	16	AAW68759	Cytotoxic T lympho
533	24	24.2	19	19	AAW61508	Peptide circ4, base	606	24	24.2	25	18	AAW32896	HIV pol protein ep
534	24	24.2	19	20	AAW27164	Mouse ST2L peptide	607	24	24.2	25	19	AAW75039	Fragment of human
535	24	24.2	19	21	AAW98289	Alpha D peptide de	608	24	24.2	25	22	AAW64846	Human brain expres
536	24	24.2	19	22	AAW98290	Alpha D peptide de	609	24	24.2	25	23	AAW30911	Amino acid sequenc
537	24	24.2	19	22	AAW47234	hmf1 Mitofusin GT	610	24	24.2	25	22	AAW68685	HIV-1 p21 peptide
538	24	24.2	19	23	AAW17770	Human beta-defensi	611	24	24.2	25	23	AAW62629	Eubacterial DnaE1
539	24	24.2	19	23	AAW93571	Granulocyte-colony	612	24	24.2	25	23	AAW67332	Omega-conopeptide
540	24	24.2	19	23	AAW73575	Vascular endotheli	613	24	24.2	25	23	AAW78615	Human Bad peptide
541	24	24.2	20	13	AAW24872	Sequence of a pep	614	24	24.2	25	23	AAW70911	Human Bad peptide
542	24	24.2	20	18	AAW26360	Erythropoietin rec	615	24	24.2	25	23	AAW80510	Histone 2A-derived
543	24	24.2	20	18	AAW13713	Erythropoietin rec	616	24	24.2	25	23	AAW43620	S. lividans protea
544	24	24.2	20	18	AAW26696	Toxoplasma gondii	617	24	24.2	16	20	AAW43620	Immunospecific pep
545	24	24.2	20	18	AAW27027	Monomer subunit of	618	24	24.2	18	22	AAW27366	Human ADP1 tryptic
546	24	24.2	20	19	AAW71650	Smooth muscle myos	619	24	24.2	22	22	AAW31977	Novel bone marrow
547	24	24.2	20	20	AAW26295	Peptide comprising	620	24	24.2	22	4	AAW30272	Novel human secret
548	24	24.2	20	21	AAW23112	Peptide wild-type A	621	24	24.2	23	6	AAW87141	Sequence of AAs 32
549	24	24.2	20	21	AAW35561	5/20 native Ara h	622	24	24.2	23	19	AAW87141	Peptide determined
550	24	24.2	20	21	AAW13297	Caenothabditis ele	623	24	24.2	23	15	AAW48438	Histogranin deriva
551	24	24.2	20	22	AAW28788	Peptide #1439 enco	624	24	24.2	7	15	AAW48477	Histogranin deriva
552	24	24.2	20	22	AAW33975	Peptide #1481 enco	625	24	24.2	7	20	AAW42046	Rheumatoid arthrit
553	24	24.2	20	22	AAW19414	Protein #1413 enco	626	24	24.2	7	21	AAW1853	Alpha-MSH analogue
554	24	24.2	20	22	AAW54738	Human brain expres	627	24	24.2	8	15	AAW48435	Histogranin deriva
555	24	24.2	20	22	AAW57132	Human bone marrow	628	24	24.2	8	17	AAW05711	Histogranin deriva
556	24	24.2	20	22	AAW14596	Peptide #1430 enco	629	24	24.2	8	19	AAW79116	Minimal motif #8.
557	24	24.2	20	22	AAW27432	Peptide #1469 enco	630	24	24.2	8	19	AAW79116	Gly-ala polymer of
558	24	24.2	20	22	AAW04774	Native anaphylacti	631	24	24.2	8	21	AAW08149	MSH-receptor subty
559	24	24.2	20	22	AAW05099	Anaphylactic peanu	632	24	24.2	9	15	AAW48437	Peptide modulating
560	24	24.2	20	22	AAW05375	R1 and R2 peptide	633	24	24.2	9	14	AAW48436	Rh/SSA epitope 84.
561	24	24.2	20	22	AAW02723	Peptide #1405 enco	634	24	24.2	9	15	AAW48432	Histogranin deriva
562	24	24.2	20	22	AAW17161	DAPPI immunogenic	635	24	24.2	9	15	AAW48471	Histogranin deriva
563	24	24.2	20	22	AAW50818	Turkey protein cal	636	24	24.2	9	15	AAW48492	Histogranin deriva
564	24	24.2	20	23	AAW36794	Human peptide enco	637	24	24.2	9	15	AAW57720	Peptide (218) inh
565	24	24.2	20	23	AAW17404	DNA binding peptid	638	24	24.2	9	15	AAW57707	Peptide (207) inh
566	24	24.2	20	23	AAW090347	Insulin/Insulin-1i	639	24	24.2	9	15	AAW57709	Peptide (209) inh
567	24	24.2	21	13	AAW27074	Recombinant xylana	640	24	24.2	9	15	AAW57693	Peptide (193) inh
568	24	24.2	21	19	AAW97205	N-terminal fragmen	641	24	24.2	9	17	AAW49388	Human leucocyte an
569	24	24.2	21	22	AAW22432	Novel human diagno	642	24	24.2	9	17	AAW12598	SH2 binding peptid
570	24	24.2	21	22	AAW55702	Peptide associated	643	24	24.2	9	17	AAW12599	SH2 binding peptid
571	24	24.2	21	22	AAW57549	Tat-CLASPcarboxyl	644	24	24.2	9	19	AAW66164	MSH-receptor subty
572	24	24.2	21	22	AAW57959	Tat-CLASPcarboxyl	645	24	24.2	9	20	AAW07472	Mouse MMAC1 gene b
573	24	24.2	21	23	AAW88608	Insulin/Insulin-1i	646	24	24.2	9	21	AAW96715	Human E3 ubiquitin
574	24	24.2	22	12	AAW11156	Hirulog-17. Synth	647	24	24.2	9	22	AAW67625	Influenza virus im
575	24	24.2	22	15	AAW47613	Bombesin-like pept	648	24	24.2	10	15	AAW38353	p53-derived HLA-bi
576	24	24.2	22	15	AAW47613	Bombesin-like pept	649	24	24.2	10	15	AAW48429	Histogranin deriva
577	24	24.2	22	20	AAW22160	Human BS135 protei	650	24	24.2	10	15	AAW48437	Histogranin deriva
578	24	24.2	22	21	AAW13646	C. trachomatis pmp	651	24	24.2	10	15	AAW48468	Histogranin deriva
579	24	24.2	22	22	AAW87914	Human Immune/haema	652	24	24.2	10	15	AAW48476	Histogranin deriva
580	24	24.2	22	22	AAW83214	PE17b expression	653	24	24.2	10	17	AAW12579	SH2 binding peptid
581	24	24.2	22	23	AAW21837	Breast tissue libt	654	24	24.2	10	17	AAW12570	SH2 binding peptid
582	24	24.2	22	23	AAW94185	Chlamydia peptide	655	24	24.2	10	18	AAW32644	Human platelet gly
583	24	24.2	22	15	AAW58462	TSAR binding domai	656	24	24.2	10	18	AAW32644	Human platelet gly
584	24	24.2	23	17	AAW89957	Rabbit eif-4-gamma	657	24	24.2	10	19	AAW17770	Minotopo capable o
585	24	24.2	23	17	AAW36404	Fragment of human	658	24	24.2	10	19	AAW17773	Minotopo capable o
586	24	24.2	23	20	AAW01040	Methylated SMD hom	659	24	24.2	10	20	AAW55308	CD34 antigen antiq
587	24	24.2	23	21	AAW19396	Kemptide phosphory	660	24	24.2	10	20	AAW45934	Immunogenic peptid
588	24	24.2	23	22	AAW829178	Peptide #1829 enco	661	24	24.2	10	20	AAW46996	Immunogenic peptid
589	24	24.2	23	22	AAW34334	Peptide #1840 enco	662	24	24.2	10	21	AAW06153	sceV 9A4 clone 23A
590	24	24.2	23	22	AAW19755	Protein #1754 enco	663	24	24.2	10	21	AAW87054	Human haematopoiet
591	24	24.2	23	22	AAW55131	Human bone marrow	664	24	24.2	10	22	AAW23947	HIV A11 motif vif
592	24	24.2	23	22	AAW65753	Human brain marrow	665	24	24.2	10	22	AAW50167	Monoclonal antibod
593	24	24.2	23	22	AAW15337	Peptide #1771 enco	666	24	24.2	10	22	AAW38827	Human complementar
594	24	24.2	23	22	AAW27814	Peptide #1851 enco	667	24	24.2	10	22	AAW38833	Human complementar

668	23	23.2	10	22	AAG5776	Human complementat	741	23	23.2	14	15	AAR48422	Histogranin deriva
669	23	23.2	10	22	AAG5827	Human complementat	742	23	23.2	14	15	AAR48461	Histogranin deriva
670	23	23.2	10	22	AAG5878	Human complementat	743	23	23.2	14	15	AAR48491	Histogranin deriva
671	23	23.2	10	22	AAG37172	Arabidopsis thalia	744	23	23.2	14	15	AAR48494	Histogranin deriva
672	23	23.2	10	22	AAG3722	Arabidopsis thalia	745	23	23.2	14	20	AAV30321	Potential T cell e
673	23	23.2	10	22	AAG3853	Arabidopsis thalia	746	23	23.2	14	20	AAV06546	Hepatocellular car
674	23	23.2	10	22	AAG3855	Arabidopsis thalia	747	23	23.2	14	20	AAV03194	Amino acid sequenc
675	23	23.2	10	22	AAG3857	Arabidopsis thalia	748	23	23.2	14	21	AAAB20728	High mobility giv
676	23	23.2	10	22	AAG3885	Arabidopsis thalia	749	23	23.2	14	21	AAAB6426	HIV A2-binding HIV
677	23	23.2	10	22	AAG3885	Arabidopsis thalia	750	23	23.2	14	22	AAAB6782	Human peptide #57
678	23	23.2	10	22	AAG3887	Arabidopsis thalia	751	23	23.2	14	22	AAAB6896	Human peptide #171
679	23	23.2	10	22	AAG3887	Arabidopsis thalia	752	23	23.2	14	22	AAAB6896	Human peptide #329
680	23	23.2	10	22	AAG3887	Arabidopsis thalia	753	23	23.2	14	22	AAAB6896	Human peptide #1174
681	23	23.2	10	22	AAG3887	Arabidopsis thalia	754	23	23.2	14	22	AAAB6896	Human peptide #1174
682	23	23.2	10	22	AAG3887	Arabidopsis thalia	755	23	23.2	14	22	AAAB6896	Human peptide #1174
683	23	23.2	10	22	AAG3887	Arabidopsis thalia	756	23	23.2	14	22	AAAB6896	Human peptide #1174
684	23	23.2	10	22	AAG3887	Arabidopsis thalia	757	23	23.2	14	22	AAAB6896	Human peptide #1174
685	23	23.2	10	22	AAG3887	Arabidopsis thalia	758	23	23.2	14	22	AAAB6896	Human peptide #1174
686	23	23.2	10	22	AAG3887	Arabidopsis thalia	759	23	23.2	14	22	AAAB6896	Human peptide #1174
687	23	23.2	10	22	AAG3887	Arabidopsis thalia	760	23	23.2	14	22	AAAB6896	Human peptide #1174
688	23	23.2	10	22	AAG3887	Arabidopsis thalia	761	23	23.2	14	22	AAAB6896	Human peptide #1174
689	23	23.2	10	22	AAG3887	Arabidopsis thalia	762	23	23.2	14	22	AAAB6896	Human peptide #1174
690	23	23.2	10	22	AAG3887	Arabidopsis thalia	763	23	23.2	14	22	AAAB6896	Human peptide #1174
691	23	23.2	10	22	AAG3887	Arabidopsis thalia	764	23	23.2	14	22	AAAB6896	Human peptide #1174
692	23	23.2	10	22	AAG3887	Arabidopsis thalia	765	23	23.2	14	22	AAAB6896	Human peptide #1174
693	23	23.2	10	22	AAG3887	Arabidopsis thalia	766	23	23.2	14	22	AAAB6896	Human peptide #1174
694	23	23.2	10	22	AAG3887	Arabidopsis thalia	767	23	23.2	14	22	AAAB6896	Human peptide #1174
695	23	23.2	10	22	AAG3887	Arabidopsis thalia	768	23	23.2	14	22	AAAB6896	Human peptide #1174
696	23	23.2	10	22	AAG3887	Arabidopsis thalia	769	23	23.2	14	22	AAAB6896	Human peptide #1174
697	23	23.2	10	22	AAG3887	Arabidopsis thalia	770	23	23.2	14	22	AAAB6896	Human peptide #1174
698	23	23.2	10	22	AAG3887	Arabidopsis thalia	771	23	23.2	14	22	AAAB6896	Human peptide #1174
699	23	23.2	10	22	AAG3887	Arabidopsis thalia	772	23	23.2	14	22	AAAB6896	Human peptide #1174
700	23	23.2	10	22	AAG3887	Arabidopsis thalia	773	23	23.2	14	22	AAAB6896	Human peptide #1174
701	23	23.2	10	22	AAG3887	Arabidopsis thalia	774	23	23.2	14	22	AAAB6896	Human peptide #1174
702	23	23.2	10	22	AAG3887	Arabidopsis thalia	775	23	23.2	14	22	AAAB6896	Human peptide #1174
703	23	23.2	10	22	AAG3887	Arabidopsis thalia	776	23	23.2	14	22	AAAB6896	Human peptide #1174
704	23	23.2	10	22	AAG3887	Arabidopsis thalia	777	23	23.2	14	22	AAAB6896	Human peptide #1174
705	23	23.2	10	22	AAG3887	Arabidopsis thalia	778	23	23.2	14	22	AAAB6896	Human peptide #1174
706	23	23.2	10	22	AAG3887	Arabidopsis thalia	779	23	23.2	14	22	AAAB6896	Human peptide #1174
707	23	23.2	10	22	AAG3887	Arabidopsis thalia	780	23	23.2	14	22	AAAB6896	Human peptide #1174
708	23	23.2	10	22	AAG3887	Arabidopsis thalia	781	23	23.2	14	22	AAAB6896	Human peptide #1174
709	23	23.2	10	22	AAG3887	Arabidopsis thalia	782	23	23.2	14	22	AAAB6896	Human peptide #1174
710	23	23.2	10	22	AAG3887	Arabidopsis thalia	783	23	23.2	14	22	AAAB6896	Human peptide #1174
711	23	23.2	10	22	AAG3887	Arabidopsis thalia	784	23	23.2	14	22	AAAB6896	Human peptide #1174
712	23	23.2	10	22	AAG3887	Arabidopsis thalia	785	23	23.2	14	22	AAAB6896	Human peptide #1174
713	23	23.2	10	22	AAG3887	Arabidopsis thalia	786	23	23.2	14	22	AAAB6896	Human peptide #1174
714	23	23.2	10	22	AAG3887	Arabidopsis thalia	787	23	23.2	14	22	AAAB6896	Human peptide #1174
715	23	23.2	10	22	AAG3887	Arabidopsis thalia	788	23	23.2	14	22	AAAB6896	Human peptide #1174
716	23	23.2	10	22	AAG3887	Arabidopsis thalia	789	23	23.2	14	22	AAAB6896	Human peptide #1174
717	23	23.2	10	22	AAG3887	Arabidopsis thalia	790	23	23.2	14	22	AAAB6896	Human peptide #1174
718	23	23.2	10	22	AAG3887	Arabidopsis thalia	791	23	23.2	14	22	AAAB6896	Human peptide #1174
719	23	23.2	10	22	AAG3887	Arabidopsis thalia	792	23	23.2	14	22	AAAB6896	Human peptide #1174
720	23	23.2	10	22	AAG3887	Arabidopsis thalia	793	23	23.2	14	22	AAAB6896	Human peptide #1174
721	23	23.2	10	22	AAG3887	Arabidopsis thalia	794	23	23.2	14	22	AAAB6896	Human peptide #1174
722	23	23.2	10	22	AAG3887	Arabidopsis thalia	795	23	23.2	14	22	AAAB6896	Human peptide #1174
723	23	23.2	10	22	AAG3887	Arabidopsis thalia	796	23	23.2	14	22	AAAB6896	Human peptide #1174
724	23	23.2	10	22	AAG3887	Arabidopsis thalia	797	23	23.2	14	22	AAAB6896	Human peptide #1174
725	23	23.2	10	22	AAG3887	Arabidopsis thalia	798	23	23.2	14	22	AAAB6896	Human peptide #1174
726	23	23.2	10	22	AAG3887	Arabidopsis thalia	799	23	23.2	14	22	AAAB6896	Human peptide #1174
727	23	23.2	10	22	AAG3887	Arabidopsis thalia	800	23	23.2	14	22	AAAB6896	Human peptide #1174
728	23	23.2	10	22	AAG3887	Arabidopsis thalia	801	23	23.2	14	22	AAAB6896	Human peptide #1174
729	23	23.2	10	22	AAG3887	Arabidopsis thalia	802	23	23.2	14	22	AAAB6896	Human peptide #1174
730	23	23.2	10	22	AAG3887	Arabidopsis thalia	803	23	23.2	14	22	AAAB6896	Human peptide #1174
731	23	23.2	10	22	AAG3887	Arabidopsis thalia	804	23	23.2	14	22	AAAB6896	Human peptide #1174
732	23	23.2	10	22	AAG3887	Arabidopsis thalia	805	23	23.2	14	22	AAAB6896	Human peptide #1174
733	23	23.2	10	22	AAG3887	Arabidopsis thalia	806	23	23.2	14	22	AAAB6896	Human peptide #1174
734	23	23.2	10	22	AAG3887	Arabidopsis thalia	807	23	23.2	14	22	AAAB6896	Human peptide #1174
735	23	23.2	10	22	AAG3887	Arabidopsis thalia	808	23	23.2	14	22	AAAB6896	Human peptide #1174
736	23	23.2	10	22	AAG3887	Arabidopsis thalia	809	23	23.2	14	22	AAAB6896	Human peptide #1174
737	23	23.2	10	22	AAG3887	Arabidopsis thalia	810	23	23.2	14	22	AAAB6896	Human peptide #1174
738	23	23.2	10	22	AAG3887	Arabidopsis thalia	811	23	23.2	14	22	AAAB6896	Human peptide #1174
739	23	23.2	10	22	AAG3887	Arabidopsis thalia	812	23	23.2	14	22	AAAB6896	Human peptide #1174
740	23	23.2	10	22	AAG3887	Arabidopsis thalia	813	23	23.2	14	22	AAAB6896	Human peptide #1174
	</												



814	23	23.2	15	22	AAB97905	Human casein Kinase
815	23	23.2	15	22	AAB58613	Altered MHC determ
816	23	23.2	15	23	ABJ01156	Human neurogenin I
817	23	23.2	15	23	ABB84101	Human single chain
818	23	23.2	15	23	AA666178	Peptide substrate
819	23	23.2	15	23	AA078700	Peptide used in an
820	23	23.2	15	23	ABB06720	Human oestrogen re
821	23	23.2	15	23	AAAM50869	Catherin 3 antigen
822	23	23.2	16	15	AAAS2095	Mouse light chain
823	23	23.2	16	15	AAAS2081	Mouse light chain
824	23	23.2	16	15	AAAS2082	Mouse light chain
825	23	23.2	16	15	AAAS2177	Human light chain
826	23	23.2	16	15	AAAS4879	Human light chain
827	23	23.2	16	15	AAAR48480	Histogranin deriva
828	23	23.2	16	15	AAAR48481	Histogranin deriva
829	23	23.2	16	15	AAAR48482	Histogranin deriva
830	23	23.2	16	15	AAAR48483	Histogranin deriva
831	23	23.2	16	15	AAAR48484	Histogranin deriva
832	23	23.2	16	15	AAAR48485	Histogranin deriva
833	23	23.2	16	15	AAAR48486	Histogranin deriva
834	23	23.2	16	15	AAAR48487	Histogranin deriva
835	23	23.2	16	15	AAAR48488	Histogranin deriva
836	23	23.2	16	15	AAAR48489	Histogranin deriva
837	23	23.2	16	15	AAAR48501	Histogranin deriva
838	23	23.2	16	18	AAAM36406	Histogranin deriva
839	23	23.2	16	18	AAAM30984	Antimicrobial prot
840	23	23.2	16	21	AAAY95422	Timothy grass poll
841	23	23.2	16	21	AAAY95423	Anti-angiotensin D3
842	23	23.2	16	21	AAAB09057	Anti-angiotensin D3
843	23	23.2	16	21	AAAY66778	Hepatitis GB virus
844	23	23.2	16	23	AAE24509	T cell antigen rec
845	23	23.2	16	23	AAE24510	Human RAR1d6 N-my
846	23	23.2	17	11	AAAR06068	Immunoreactive pep
847	23	23.2	17	11	AAAR06072	Immunoreactive pep
848	23	23.2	17	15	AAAR48440	Histogranin deriva
849	23	23.2	17	15	AAAR48441	Histogranin deriva
850	23	23.2	17	15	AAAR48442	Histogranin deriva
851	23	23.2	17	15	AAAR48443	Histogranin deriva
852	23	23.2	17	15	AAAR48444	Histogranin deriva
853	23	23.2	17	15	AAAR48445	Histogranin deriva
854	23	23.2	17	15	AAAR48446	Histogranin deriva
855	23	23.2	17	15	AAAR48447	Histogranin deriva
856	23	23.2	17	15	AAAR48448	Histogranin deriva
857	23	23.2	17	15	AAAR48449	Histogranin deriva
858	23	23.2	17	15	AAAR48450	Histogranin deriva
859	23	23.2	17	20	AAAY42455	Parasin I syntheti
860	23	23.2	17	22	AAAB06321	Human substrate-ke
861	23	23.2	17	22	AAAG67712	Peptide HBp6 deriv
862	23	23.2	17	22	AAAB60552	Rat ghrelin fragme
863	23	23.2	18	14	AAAR40151	Lactate dehydrogen
864	23	23.2	18	15	AAAR47401	PDGF-activity-disp
865	23	23.2	18	15	AAAR47796	HIV epitope #127.
866	23	23.2	18	15	AAAR62133	UL-1 beta nonpept
867	23	23.2	18	16	AAAR74788	Variant h of C-ter
868	23	23.2	18	16	AAAR72412	Variant g of C-ter
869	23	23.2	18	16	AAAR72411	Rat NDF-alpha2 N-t
870	23	23.2	18	17	AAAR68598	Leader sequence fo
871	23	23.2	18	17	AAAR86162	An oxidant scaveng
872	23	23.2	18	18	AAAM32598	Cyclic peptide of
873	23	23.2	18	18	AAAM52560	Amino acid sequenc
874	23	23.2	18	20	AAAM46344	Antimicrobial cycl
875	23	23.2	18	20	AAAY17367	Mus musculus haema
876	23	23.2	18	20	AAAM95558	C-terminal peptide
877	23	23.2	18	21	AAAY94792	Synthetic SKI-1 pr
878	23	23.2	18	21	AAAB06286	Human substrate-ke
879	23	23.2	18	21	AAAB06320	Hepatitis GB virus
880	23	23.2	18	22	ABG30120	Novel human diagno
881	23	23.2	18	22	ABB33584	Peptide #7090 enco
882	23	23.2	18	22	AAAG67717	D-form peptide of
883	23	23.2	18	22	AAAG67718	Modified peptide H
884	23	23.2	18	22	AAAG67738	Human brain expres
885	23	23.2	18	22	AAAG67738	
886	23	23.2	18	22	AAAM60070	
887	23	23.2	18	22	AAAM60283	Human brain expres
888	23	23.2	18	22	AAAM72678	Human bone marrow
889	23	23.2	18	22	AAAM72912	Human bone marrow
890	23	23.2	18	22	AAAM32909	Peptide #6946 enco
891	23	23.2	18	22	AAAM33143	Peptide #7180 enco
892	23	23.2	18	22	AAE05534	CD40-binding txpe
893	23	23.2	18	22	AAAG80794	CD40-repressor SH3
894	23	23.2	18	22	AAAG80796	C diphtheriae DtxR
895	23	23.2	18	22	AAAB60553	Rat ghrelin fragme
896	23	23.2	18	22	AAAB50504	CD40-binding pepit
897	23	23.2	18	23	ABGA42747	Human peptide enco
898	23	23.2	18	23	ABGA42747	Human peptide enco
899	23	23.2	18	23	AAE19025	Human ghrelin pepit
900	23	23.2	18	23	AAE15413	Human PDGF-A matr1
901	23	23.2	19	11	AAAR07750	Human PDGF-A matr1
902	23	23.2	19	11	AAAR34049	Lytic peptide with
903	23	23.2	19	16	AAAR82623	HCV NS peptide DP5
904	23	23.2	19	16	AAAR79366	70K autoantigen pe
905	23	23.2	19	17	AAAR97641	Thrombospondin hep
906	23	23.2	19	17	AAAY06693	Cell binding domai
907	23	23.2	19	19	AAAM9102	Human neurofilamen
908	23	23.2	19	20	AAAY12454	Human topoisomeras
909	23	23.2	19	21	AAAB30178	Parasin I amino ac
910	23	23.2	19	21	AAAY90725	Cytochemical assay
911	23	23.2	19	21	AAAY70906	Influenza haemaggl
912	23	23.2	19	22	AAAG67739	Synthetic peptide,
913	23	23.2	19	22	AAAG67739	Modified peptide H
914	23	23.2	19	22	AAAB08619	Interleukin-1 inh1
915	23	23.2	19	22	AAAB62656	Human z51933 pepti
916	23	23.2	19	22	AAAB65340	Alpha3beta1 integr
917	23	23.2	19	22	AAAB60554	Rat ghrelin fragme
918	23	23.2	19	23	AAU72613	T cell receptor im
919	23	23.2	20	13	AAAR28289	Hi-30 N-terminal s
920	23	23.2	20	14	AAAR35455	Delta TCR V-J junc
921	23	23.2	20	15	AAAR47396	PDGF-activity-disp
922	23	23.2	20	15	AAAR47400	PDGF-activity-disp
923	23	23.2	20	17	AAAM16990	ABL SH3 domain-bin
924	23	23.2	20	17	AAAR91032	R6 linker peptide.
925	23	23.2	20	18	AAAM42903	Immunogenic Hepati
926	23	23.2	20	18	AAAM68650	Helicobacter pylori
927	23	23.2	20	21	AAAB36363	Bacillus subtilis
928	23	23.2	20	21	AAAB13673	C. trachomatis OMC
929	23	23.2	20	21	AAAY1045	CLN3 peptide seque
930	23	23.2	20	21	AAAY84265	Truncated macropha
931	23	23.2	20	22	AAAC83241	Chlamydia trachoma
932	23	23.2	20	22	AAAB60555	Insulin/Insulin-II
933	23	23.2	20	23	AAU90320	Rat ghrelin fragme
934	23	23.2	20	23	AAU90404	Insulin/Insulin-II
935	23	23.2	20	23	ABBS94212	Insulin/Insulin-II
936	23	23.2	20	23	AAU85556	Chlamydia peptide
937	23	23.2	21	14	AAAR39856	Lung tumour protei
938	23	23.2	21	19	AAAR75732	E2 peptide E2-4, r
939	23	23.2	21	21	AAAB34858	Proline/Arginine r
940	23	23.2	21	21	AAAB31919	Human secreted pro
941	23	23.2	21	22	ABBS7154	Peptide #4570 enco
942	23	23.2	21	22	ABBS22464	Peptide #4660 enco
943	23	23.2	21	22	AAAM7869	Protein #4463 enco
944	23	23.2	21	22	AAAM55593	Human brain expres
945	23	23.2	21	22	AAAM70293	Human brain expres
946	23	23.2	21	22	AAAM18123	Human bone marrow
947	23	23.2	21	22	AAAM30650	Peptide #4557 enco
948	23	23.2	21	22	AAAM38491	Peptide #4667 enco
949	23	23.2	21	22	AAAM05756	Peptide #12528 enc
950	23	23.2	21	22	AAAB60556	Peptide #4438 enco
951	23	23.2	21	22	ABG39933	Rat ghrelin fragme
952	23	23.2	21	23	ABG39933	Synthetic HAV VP3
953	23	23.2	21	23	AAU88186	Human peptide enco
954	23	23.2	21	23	AAU88331	Insulin/Insulin-II
955	23	23.2	21	23	AAU88331	Insulin/Insulin-II
956	23	23.2	21	23	AAU89756	Insulin/Insulin-II
957	23	23.2	21	23	AAU89753	Insulin/Insulin-II
958	23	23.2	21	23	AAU72655	Insulin/Insulin-II
959	23	23.2	21	23	AAU72655	T cell receptor. Im
	23	23.2	22	19	AAU20359	Human microtubule
	23	23.2	22	19	AAAM69871	Exosite associatin

960 23 23.2 22 19 AAM56045  
 961 23 23.2 22 19 AAM50187  
 962 23 23.2 22 20 AAY04031  
 963 23 23.2 22 20 AAY04038  
 964 23 23.2 22 21 AAB23922  
 965 23 23.2 22 21 AAY84560  
 966 23 23.2 22 21 AAY52080  
 967 23 23.2 22 21 AAY52081  
 968 23 23.2 22 21 AAY52082  
 969 23 23.2 22 21 AAY56472  
 970 23 23.2 22 21 AAY73163  
 971 23 23.2 22 21 AAY66995  
 972 23 23.2 22 22 ABB27986  
 973 23 23.2 22 22 ABB28918  
 974 23 23.2 22 22 ABB33158  
 975 23 23.2 22 22 ABB18623  
 976 23 23.2 22 22 ABB20518  
 977 23 23.2 22 22 AAM53954  
 978 23 23.2 22 22 AAM55921  
 979 23 23.2 22 22 AAM66342  
 980 23 23.2 22 22 AAM68290  
 981 23 23.2 22 22 AAM14211  
 982 23 23.2 22 22 AAM16113  
 983 23 23.2 22 22 AAM26621  
 984 23 23.2 22 22 AAM28604  
 985 23 23.2 22 22 AAM01943  
 986 23 23.2 22 22 AAM03838  
 987 23 23.2 22 22 AAB60557  
 988 23 23.2 22 22 AAB51676  
 989 23 23.2 22 23 AABG35990  
 990 23 23.2 22 23 AABG37835  
 991 23 23.2 22 23 AAU81916  
 992 23 23.2 23 15 AAR65373  
 993 23 23.2 23 17 AAR90958  
 994 23 23.2 23 19 AAY21068  
 995 23 23.2 23 20 AAY28956  
 996 23 23.2 23 20 AAY28958  
 997 23 23.2 23 20 AAY19774  
 998 23 23.2 23 20 AAM67910  
 999 23 23.2 23 21 AAB23983  
 1000 23 23.2 23 21 AAY87142

## ALIGNMENTS

## RESULT 1

56391  
 AAY56391 standard; peptide; 19 AA.

AC AAY56391;  
 DT 15-FEB-2000 (first entry)

DE Mutant beta-APP protein peptide sequence SEQ ID NO:1.

XX Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;  
 KW Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;  
 KM gene therapy.

OS Synthetic.  
 OS Homo sapiens.

PN WC0958564-A1.

PD 18-NOV-1999.

PF 30-APR-1999; 99WO-NO00141.

PR 08-MAY-1998; 98NO-0002098.

PA (NHVD) NORSK HYDRO AS.

Chimeric adenovirus  
 Monoclonal antibody  
 HIV-1 p24 peptide  
 HIV-1 p24 peptide  
 TRMP-2 derived ant  
 Antigenic peptide  
 E. coli DP3 prote  
 S. typhimurium DP3  
 Protein fragment D  
 Synthetic p53 pep  
 HIV-derived MHC cl  
 BAX mutant peptide  
 Human peptide #637  
 Peptide #2569 enco  
 Peptide #664 enco  
 Peptide #622 enco  
 Protein #2517 enco  
 Human brain expres  
 Human brain expres  
 Human bone marrow  
 Human bone marrow  
 Peptide #645 enco  
 Peptide #2547 enco  
 Peptide #658 enco  
 Peptide #2641 enco  
 Peptide #625 enco  
 Peptide #2520 enco  
 Rat ghrelin fragme  
 Anti-tetanus toxoi  
 Human peptide enco  
 Human peptide enco  
 Bacillus thuringie  
 Helper T cell epit  
 Factor VIII antige  
 Human p53 cellular  
 Amino acid sequenc  
 Amino acid sequenc  
 SEQ ID NO 492 from  
 Human secreted pro  
 Peptide amino acid  
 Human secreted pro

PI Gaudernack G, Eriksen JA, Moller M;  
 XX WPI: 2000-039070/03.  
 DR  
 XX  
 PT Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,  
 PR useful for treating Alzheimer's disease and Down syndrome  
 PS Claim 10; Page 27; 33pp; English.  
 CC The present invention describes frameshift mutant beta-amyloid precursor  
 CC peptides (beta-APP) (AAY56391 to AAY56394) and mutant ubiquitin-B  
 CC (Ubi-B) (AAY56395 to AAY56400) associated with Alzheimer's disease and  
 CC Down syndrome eliciting T cellular immunity. The peptides may be used as  
 CC a vaccine for Alzheimer's disease and Down syndrome. The vaccination is  
 CC sufficient to induce specific T-cell immunity to mutant beta-APP and/or  
 CC Ubi-B peptides that are associated with Alzheimer's disease or Down  
 CC syndrome. The patient may be stimulated in vivo or ex vivo with the  
 CC peptides. The peptides and DNA encoding the peptides can also be used for  
 CC the treatment or prophylaxis of Alzheimer's disease or the treatment of  
 CC Down syndrome.  
 XX  
 SQ Sequence 19 AA;  
 Query Match 100.0%; Score 99; DB 21; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1,6e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NVPGHERMGRGRTSKELA 19

Db 1 NVPGHERMGRGRTSKELA 19

## RESULT 2

AAY20219 standard; Protein; 25 AA.

AC AAY20219;

DT 22-JUL-1999 (first entry)

DE Human beta-amyloid precursor protein mutant fragment 44.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 KW frameshift mutation; age-related disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 KW high mobility group protein-C; neuroendocrine specific protein A.

OS Synthetic.

OS Homo sapiens.

PN WC09845322-A2

PD 15-OCT-1998.

PF 02-APR-1998; 98WO-IB00705.

PR 10-APR-1997; 97US-0043163.

PA (UYUT-) RIJKSUNIV UTRECHT.

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PI Burbach JPH, Grosveld FG, Van Leeuwen FW;

DR WPI: 1998-609901/51.

DR N-PSDB; AAX75753.

Disclosure; Figure 2; 258pp; English.

Sequence 25 AA;

```
QY 1 NVPCHERMGRGRTSSKELA 19
    |||||
Db 7 NVPCHERMGRGRTSSKELA 25
```

AAB99216;

AMY6 peptide.

Unidentified.

07-JUN-2001.

04-DEC-2000;

03-DEC-1999-

NEW YORK ROUTE

HOL EM, Van Leeuwen FW;

WPI: 2001-397965/42.

## Detecting a disease

**PT** Detecting a disease or pathological condition, associated with secretion of aberrant protein e.g. age-related diseases, by determining

Disclosure; Page 24; .36pp; English.

Sequence 19 AA.

```
QY 1 NVPHERMGRTSSKELA 19
    ||| ||| ||| ||| |||
Db 2 NVP-HERMGRTSSKELA 19
```

AAB99215

AMY5 peptide

Unidentified.

07-JUN-2001.

04-DEC-2000: 20

03-DEC-1999.

# REPORT & RECOMMENDATIONS

NOT RECORDED

WPL; 2001-39/96

PT Detecting a disease or pathological condition, associated with

PT secretion of aberrant protein e.g. age-related diseases, by determining  
PT level of aberrant protein and/or its detectable part in body fluid  
PT and/or tissue -

aa Disclosure; Page 24; 36pp; English.

The present invention relates to method for detecting a disease or pathological condition associated with molecular misreading of coding sequences in the genome and/or associated with the clearance of aberrant protein. The method comprises providing a sample of a body fluid and/or tissue of a patient and determining a level of the aberrant protein and/or its detectable part or the ratio between the two in the body fluid and/or tissue. The method enables diagnosing the disease before the patient exhibits clinical symptoms. The method is useful for diagnosing age-related diseases, preferably Alzheimer's disease, Down's syndrome or other age related diseases e.g. cancer; neurodegenerative diseases, such as frontal lobe dementia, progressive supranuclear palsy; and other diseases with abundant tau-positive filamentous lesions, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease, spinocerebellar ataxia-3, multiple sclerosis; other inclusion body diseases associated with ubiquitin, diabetes mellitus type II and other degenerative diseases such as cardiovascular diseases and rheumatoid arthritis. A number of other diseases which can be diagnosed are given in the specification. The present sequence is Amy 5 peptide, which was coupled to thyroglobulin by glutaraldehyde, and used to immunise rabbits for antibody production in the present invention. The Amy 5 peptide is a C-terminal fragment of the full-length beta-amyloid precursor protein (APP+1; mature APP and its signal peptide) protein.

AA	Sequence	14 AA;
SQ		

Query Match	63.6%;	Score 63;	DB 22;	Length 14;
Best Local Similarity	100.0%;	Pred. No.	0.00028;	

```

best local similarity: 100.00; local: not interested;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

7 RMGRCRTSSKELA 19 QY

2 RMGRGRTSSKELA 14  
Db

RESULT 5  
AAV56394  
ID AAV56394 standard: peptide: 12 AA.

DT 15-FEB-2000 (first entry)

Mutant beta-APP protein peptide sequence SEQ ID NO:4

KW Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;  
KW Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective  
KW gene therapy.

OS Synthetic.

Homo sapiens.

PN W09958564-A1.

AA  
PD  
18-NOV-1999.

30-APR-1999: 99WO-NO00141.

08-MAY-1998: 98NO-0002098.

PA (NHYD ) NORSK HYDRO AS.

XX Gaundernack G, Eriksen JA, Møller M:  
PI

XX  
DB WPT: 2000-039070/03

AA Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides  
PT useful for treating Alzheimer's disease and Down syndrome -

XX  
PS Claim 10; Page 27; 33pp; English.

AA The present invention describes frameshift mutant beta-amyloid precursor  
AB peptides (beta-APP) (AAV56391 to AAV56394) and mutant ubiquitin-B  
CC peptides (beta-UB) (AAV56400) associated with Alzheimer's disease and  
CC (Ubi-18) (AAV56395 to AAV56400) associated with Alzheimer's disease and  
CC Down syndrome eliciting T cellular immunity. The peptides may be used as  
CC a vaccine for Alzheimer's disease and Down syndrome. The vaccination is  
CC sufficient to induce specific T-cell immunity to mutant beta-APP and/or  
CC Ubi-B peptides that are associated with Alzheimer's disease or Down  
CC syndrome. The patient may be stimulated in vivo or ex vivo with the  
CC peptides. The peptides and DNA encoding the peptides can also be used for  
CC the treatment or prophylaxis of Alzheimer's disease or the treatment of  
CC Down syndrome.

aa	Sequence	12 AA;
50		

Query Match	58.6%	Score 58;	DB 21;	Length 12;
Best Local Similarity	100.0%;	Pred.No. 0.0018;		
Matches 12; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

QY 8 MGRGRTSSKELA 19

Db 1 MGRGRTSSKELA 12

RESULT 6  
AAV56393  
ID AAV56393 standard; peptide; 17 AA

AA 15-FEB-2000 (first entry)  
DT

DE	Mutant beta-APP protein peptide sequence	SEQ ID NO:3.
aa		

KW Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;  
KW Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;  
KW gene therapy.

OS Synthetic.

Homo sapiens.

PN W09958564-A1.

PD 18-NOV-1999.

AA 30-APR-1999; 99WO-NO00141.  
PF

AA 08-MAY-1998; 98NO-0002098.  
PR

AA  
PA (NHYD ) NORSK HYDRO AS.

xx Gaudernack G, Eriksen JA, Møller M;  
PT

XX  
DR  
WPT: 2000-039070/03.

AA Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides  
 PT useful for treating Alzheimer's disease and Down syndrome -

XX  
PS  
Claim 10: Page 27: 33pp: English

AA The present invention describes frameshift mutant beta-amyloid precursor  
CC peptides (beta-APP) (AAV56391 to AAV56394) and mutant ubiquitin-B  
CC (Ubi-B) (AAV56395 to AAV56400) associated with Alzheimer's disease and  
CC Down syndrome eliciting T cellular immunity. The peptides may be used as  
CC a vaccine for Alzheimer's disease and Down syndrome. The vaccination is  
CC sufficient to induce specific T-cell immunity to mutant beta-APP and/or  
CC Ubi-B peptides that are associated with Alzheimer's disease or Down  
CC syndrome. The patient may be stimulated in vivo or ex vivo with the  
CC peptides. The peptides and DNA encoding the peptides can also be used for  
CC the treatment or prophylaxis of Alzheimer's disease or the treatment of  
CC Down syndrome.

XX Sequence 17 AA; 52.5%; Score 52; DB 21; Length 17;  
 SQ Query Match Best Local Similarity 100.0%; Pred. No. 0.031;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NVPGERMG 9  
 |||||  
 Db 9 NVPGERMG 17

RESULT 7  
 AAM18633 standard; peptide: 10 AA.

XX AAM18633;  
 XX 21-JUL-1997 (first entry)

XX Peptide resulting from human amyloid A4 gene +1 frameshift mutation.  
 XX Frameshift mutation product: GACA motif; somatic mutation; diagnosis;  
 XX detection; antibody; probe; cancer; neoplasia; neurodegenerative;  
 XX Parkinson's; Alzheimer's disease; Pick's; Huntington's disease;  
 XX Down's syndrome; frontal lobe dementia; progressive supranuclear palsy;  
 XX PSP; amyotrophic lateral sclerosis; multiple sclerosis; MS;  
 XX cardiovascular; rheumatoid arthritis.  
 XX Homo sapiens.  
 XX W09712992-A2.  
 XX 10-APR-1997.  
 XX 02-OCT-1996; 96MO-IB01106.  
 XX 11-JAN-1996; 96US-0009832.  
 XX 02-OCT-1995; 95GB-0020080.  
 XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
 XX (UYRO-) ROYAL ROTTERDAM ERASMUS.  
 XX (UYUR-) UNIV STATE UTRECHT.  
 XX Burbach JPH, Grosveld FG, Van Leeuwen FW;  
 WPI: 1997-226235/20.  
 XX Use of mutant genes having frameshift mutation(s) - for developing  
 XX prods. for the diagnosis, prevention and treatment of associated  
 XX diseases, e.g. cancer or neurodegenerative disease

XX Claim 24; Page 82; 123pp; English.

XX AAM18633-W18641 are antigenic peptide products of +1 and +2 frameshift  
 XX mutations of various human genes including the amyloid A4, tau,  
 XX ubiquitin, apolipoprotein E, microtubule-associated protein 2  
 XX (MAP-2) and neurofilament subunit L, M and H genes. The peptides  
 XX are used for the production of antibodies which can be used in the  
 XX diagnosis, prevention and treatment of diseases such as cancer or  
 XX neurodegenerative disease, e.g. Parkinson's disease, Alzheimer's disease  
 XX Down's syndrome, frontal lobe dementia (Pick's disease), progressive  
 XX supranuclear palsy (PSP), amyotrophic lateral sclerosis, Huntington's  
 XX disease, multiple sclerosis, and other degenerative diseases such as  
 XX cardiovascular diseases and rheumatoid arthritis.

XX Sequence 10 AA;  
 OY Query Match 47.5%; Score 47; DB 18; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 10 RGRTSSKELA 19

Db |||||  
 1 RGRTSSKELA 10

RESULT 8  
 AAY20152  
 ID AAY20152 standard; peptide: 10 AA.  
 XX AAY20152;  
 XX 22-JUL-1999 (first entry)

XX Human beta-Ap4 immunogenic peptide fragment.  
 XX Human: beta-amyloid precursor protein; beta-Ap4; diagnosis; cancer;  
 XX frameshift mutation; age-related disease; neurodegenerative disorder;  
 XX Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 XX Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 XX diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 XX ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 XX neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 XX glial fibrillary acidic protein; GFAP; p53; semaphorin II; HUPF-1;  
 XX bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 XX high mobility group protein-C; neuroendocrine specific protein A;  
 XX immunogenic.  
 XX Homo sapiens.  
 XX W09845322-A2.  
 XX 15-OCT-1998.  
 XX 02-APR-1998; 98MO-IB00705.  
 XX 10-APR-1997; 97US-0043163.  
 XX (UYUT-) RIJKSUNIV UTRECHT.  
 XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
 XX (UYRO-) UNIV ROTTERDAM ERASMUS.  
 XX Burbach JPH, Grosveld FG, Van Leeuwen FW;  
 WPI: 1998-609901/51.  
 XX Diagnosing disease by detecting frameshift mutations in RNA or  
 XX corresponding protein mutations - used to diagnose cancer and  
 XX neurological diseases, particularly Alzheimer's disease, and also  
 XX for treatment and prevention with specific ribozymes or wild-type  
 XX RNA

XX Claim 24; Page 85; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease  
 XX caused by, or associated with, an RNA molecule that has a frameshift  
 XX mutation. The method is used to diagnose age-related diseases, especially  
 XX cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
 XX disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
 XX multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
 XX and many others listed) or susceptibility to these disorders. The method  
 XX allows a definitive diagnosis of Alzheimer's disease in living patients,  
 XX at an early stage. It is based on the observation that disease may be  
 XX caused by mutations in RNA rather than DNA. The invention describes the  
 XX use of neuronal system RNA molecules, specifically proteins including  
 XX beta-amyloid precursor protein (beta-Ap4), the microtubule associated  
 XX proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
 XX associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 XX neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
 XX protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
 XX 2 (bcl-2) proto-oncogene, semaphorin II, HUPF-1, high mobility group  
 XX protein-C (HMGP-C) and neuroendocrine specific protein A.

XX Sequence 10 AA;

Query Match 47.5%; Score 47; DB 19; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 RGRSSKELA 19  
| | | | | | | | | |  
Db 1 RGRSSKELA 10

## RESULT 9

AAB99214 ID AAB99214 standard; peptide; 10 AA.

AC AAB99214;

DT 06-SEP-2001 (first entry)

DE AMY1 peptide.

AMY1: disease detection; age-related disease; Alzheimer's disease;  
Down's syndrome; cancer; neurodegenerative disease; Parkinson's disease;  
amyotrophic lateral sclerosis; Huntington's disease; diabetes mellitus type II;  
spino cerebellar ataxia-3; multiple sclerosis; rheumatoid arthritis;  
beta-amyloid precursor protein; APP.

Unidentified.

WO200140804-A2.

PD 07-JUN-2001.

PF 04-DEC-2000; 2000MO-NL00887.

PR 03-DEC-1999; 99EP-0204140.

PA (NEW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.

PI Hol EM, Van Leeuwen FW;

DR WPI; 2001-397965/42.

PT Detecting a disease or pathological condition, associated with  
secretion of aberrant protein e.g. age-related diseases, by determining  
PT level of aberrant protein and/or its detectable part in body fluid  
PT and/or tissue -

XX Disclosure; Page 24; 36pp; English.

CC The present invention relates to a method for detecting a disease or  
CC pathological condition associated with molecular misreading of coding  
CC sequences in the genome and/or associated with the clearance of aberrant  
CC protein. The method comprises providing a sample of a body fluid and/or  
CC tissue of a patient and determining a level of the aberrant protein  
CC and/or its detectable part or the ratio between the two in the body fluid  
CC and/or tissue. The method enables diagnosing the disease before the  
CC patient exhibits clinical symptoms. The method is useful for diagnosing  
CC age-related diseases, preferably Alzheimer's disease, Down's syndrome or  
CC other age related diseases e.g. cancer; neurodegenerative diseases, such  
CC as frontal lobe dementia, progressive supranuclear palsy; and other  
CC diseases with abundant tau-positive filamentous lesions, Parkinson's  
CC disease, amyotrophic lateral sclerosis, Huntington's disease,  
CC spino cerebellar ataxia-3, multiple sclerosis; other inclusion body  
CC diseases associated with ubiquitin, diabetes mellitus type II and other  
CC degenerative diseases such as cardiovascular diseases and rheumatoid  
CC arthritis. A number of other diseases which can be diagnosed are given in  
CC the specification. The present sequence is AMY 1 peptide, which was  
CC coupled to thyroglobulin by glutaraldehyde, and used to immunise  
CC rabbits for antibody production in the present invention. The AMY 1  
CC peptide is a C-terminal fragment of the full-length beta-amyloid  
CC precursor protein (APP+1, mature APP and its signal peptide) protein.

XX Sequence 10 AA;

Query Match 47.5%; Score 47; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 RGRSSKELA 19  
| | | | | | | | | |  
Db 1 RGRSSKELA 10

## RESULT 10

AAV56395 ID AAV56395 standard; peptide; 15 AA.

AC AAV56395;

DT 15-FEB-2000 (first entry)

DE Mutant ubiquitin-B peptide sequence SEQ ID NO:5.

KW Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;

KW Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;

KW gene therapy.

OS Synthetic.

OS Homo sapiens.

PN WO958564-A1.

PD 18-NOV-1999.

PF 30-APR-1999; 99MO-NO00141.

PR 08-MAY-1998; 98MO-0002098.

PA (NHVD ) NORSK HYDRO AS.

PI Gaudernack G, Eriksen JA, Moller M;

DR WPI; 2000-039070/03.

PT Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,  
PT useful for treating Alzheimer's disease and Down syndrome -

PS Claim 10; Page 27; 33pp; English.

XX The present invention describes frameshift mutant beta-amyloid precursor  
CC peptides (beta-APP) (AAV56391 to AAV56394) and mutant ubiquitin-B  
CC (UBI-B) (AAV56395 to AAV56400) associated with Alzheimer's disease and  
CC Down syndrome eliciting T cellular immunity. The peptides may be used as  
CC a vaccine for Alzheimer's disease and Down syndrome. The vaccination is  
CC sufficient to induce specific T-cell immunity to mutant beta-APP and/or  
CC UBI-B peptides that are associated with Alzheimer's disease or Down  
CC syndrome. The patient may be stimulated in vivo or ex vivo with the  
CC peptides. The peptides and DNA encoding the peptides can also be used for  
CC the treatment or prophylaxis of Alzheimer's disease or the treatment of  
CC Down syndrome.

XX Sequence 15 AA;

Query Match 41.4%; Score 41; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RMGRGRTS 14  
| | | | | | | | | |  
Db 8 RMGRGRTS 15

## RESULT 11

AAAB48661 ID AAB48661 standard; peptide; 24 AA.

XX

AC AAB48661:  
 XX  
 DT 09-MAR-2001 (first entry).  
 XX  
 DE Human zvegfg4 peptide SEQ ID NO:41 used in antibody preparation.  
 XX  
 KW Human; zvegfg4; growth factor homologue; VEGF/PDGF family;  
 KW CUB domain; PDGF-like activity; mitogenic; osteogenic; antibody;  
 KW neovascularisation; tissue repair; proliferation; differentiation;  
 KW liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis;  
 KW periodontal disease; bone fracture; wound healing; vulnerrary; ischaemia;  
 KW immunomodulation; hepatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20006736-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 03-MAY-2000; 2000MO-US40047.  
 XX  
 PR 03-MAY-1999; 99US-0304216.  
 XX 10-NOV-1999; 99US-0164463.  
 PR 04-FEB-2000; 2000US-0180169.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;  
 XX  
 DR WPI; 2000-687541/67.  
 XX  
 PT Growth factor homologs and the nucleic acids that encode them, useful  
 PT e.g. for treating liver damage, ischemia, multiple sclerosis and  
 PT Alzheimer's disease -  
 XX  
 PS Example 9; Page 72; 143pp; English.  
 XX  
 CC The invention relates to the human growth factor homologue zvegfg4  
 CC (AAB48663), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member  
 CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial  
 CC growth factor) family. Zvegfg4 has a growth factor domain (AAB48654)  
 CC characterised by a PDGF cysteine knot structure, and a CUB domain  
 CC (AAB48655) which has a beta barrel structure. Zvegfg4 has PDGF-like  
 CC activity, having mitogenic activity on fibroblasts, vascular smooth  
 CC muscle cells and pericytes, and has also been shown to stimulate bone  
 CC growth. The invention also relates to fusion proteins comprising human  
 CC zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3  
 CC fusions; expression constructs and host cells comprising human zvegfg4  
 CC nucleic acids; the recombinant expression of human zvegfg4; an antibody  
 CC which binds to human zvegfg4 or a fragment thereof; a method of activating  
 CC a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a  
 CC method of modulating the proliferation, differentiation, migration or  
 CC metabolism of bone cells, comprising exposing bone cells to  
 CC zvegfg4-derived polypeptides; and a method of detecting a genetic  
 CC abnormality in the zvegfg4 gene of a patient. Zvegfg4 proteins and derived  
 CC fragments may be used to stimulate tissue development or repair, or  
 CC cellular differentiation or proliferation. They are particularly used for  
 CC the treatment or repair of liver damage, and may also be used to  
 CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or  
 CC multiple sclerosis). Due to their osteogenic activity, they may be used  
 CC in the treatment of periodontal disease and fractures. They may also be  
 CC used to enhance expansion and mobilisation of haematopoietic stem cells  
 CC and endothelial precursor stem cells, which may be useful in the  
 CC treatment of ischemia, in wound healing, and in the modulation of the  
 CC immune system. The present sequence represents a human zvegfg4 peptide  
 CC used to raise antibodies in an exemplification of the invention.  
 XX  
 SQ Sequence 24 AA:

Query Match 33.8%; Score 33.5; DB 21; Length 24;  
 Best Local Similarity 58.3%; Pred. No. 84;  
 Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Oy 3 PGH-ERMGRGT 13  
 DB 4 PGHKKRRGAKT 15

## RESULT 12

AAG65607  
 ID AAG65607 standard; peptide; 24 AA.  
 XX  
 AC AAG65607;  
 XX

DT 07-JAN-2002 (first entry)  
 XX

DE Human zvegfg4 peptide epitope huzvegfg4-3.  
 XX

KW Zvegfg4; bone; ligament; cartilage; osteoblast; osteoclast; chondrocyte;  
 KW bone cancer; osteonecrosis; bone defect; osteogenesis; osteoporosis;  
 KW osteopathic; vulnerrary; human; epitope.  
 XX

OS Homo sapiens.  
 XX

PN WO200157083-A1.  
 XX

PD 09-AUG-2001.  
 XX

PF 03-MAY-2000; 2000MO-US12095.  
 XX

PR 04-FEB-2000; 2000US-180169P.  
 XX 31-MAR-2000; 2000US-0540224.  
 XX

PA (ZYMO ) ZYMOGENETICS INC.  
 XX

PI Gilbertson DG, Hart CE;  
 XX

DR WPI; 2001-611088/70.  
 XX

PT Use of zvegfg4 polypeptide for promoting bone, ligament or cartilage  
 PT growth in mammal at site of fracture, implant, and bone graft, and for  
 PT promoting growth or differentiation of osteoblasts, chondrocytes in  
 PT culture -  
 XX

PS Example 3; Page 23; 57pp; English.  
 XX

CC The invention relates to the use of zvegfg4 polypeptide for promoting  
 CC bone, ligament or cartilage growth in a mammal, and for promoting  
 CC proliferation or differentiation of osteoblasts, osteoclasts,  
 CC chondrocytes or bone marrow stem cells in culture. For promoting  
 CC cartilage growth, chondrocytes are cultured ex vivo in presence of the  
 CC zvegfg4 polypeptide and then placed into mammal where cartilage is to be  
 CC grown. Zvegfg4 polypeptide is useful for promoting growth of bone,  
 CC ligament or cartilage in a mammal at a site of bony defect such as  
 CC fracture, bone graft, implant or periodontal pocket, in humans and non-  
 CC human animals such as domestic animals including livestock and companion  
 CC animals. Zvegfg4 is used for promoting growth of bone, ligament, or  
 CC cartilage in conditions of bone defects following therapeutic treatments  
 CC of bone cancers or other conditions characterized by increased bone loss  
 CC or decreased bone formation, or elevation of peak bone mass in pre-  
 CC menopausal woman. It is also useful for healing bone following radiation  
 CC -induced osteonecrosis, repairing bone defects arising from surgery, and  
 CC promotion of bone healing in plastic surgery, increasing bone formation  
 CC during distraction osteogenesis, treating bone injuries including repair  
 CC of cartilage and ligament and treatment of osteoporosis. Sequences  
 CC AAG65605-07 represents peptide epitopes of human zvegfg4 polypeptide,  
 CC used for raising rabbit polyclonal antibodies.  
 XX

SQ Sequence 24 AA:

Query Match 33.8%; Score 33.5; DB 22; Length 24;  
 Best Local Similarity 58.3%; Pred. No. 84;  
 Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
 Oy 3 PGH-ERMGRGT 13  
 III : I I I I I

Db 4 PGHRRGRAKT 15

RESULT 13

ABP51644

ID ABP51644 standard; Peptide; 24 AA.

XX

AC ABP51644;

XX

DT 30-SEP-2002. (first entry)

XX

DE Human zvegff4 peptide huzvegff4-3 SEQ ID NO:11.

XX

KW Human; zvegff4; cell proliferation; extracellular matrix production; fibroproliferative disorder; PDGF-D; platelet derived growth factor; PDGF; vascular endothelial growth factor; VEGF; cystostatic; nephrotropic; hepatotropic; antiinflammatory; osteopathic; arthritic; metastasis; prostate tumour; prostate cancer; glomerulonephritis; lupus nephritis; diabetic glomerulosclerosis; renal arteriosclerosis; nephrotic syndrome; chronic active hepatitis; cirrhosis; osteopetrosis; osteosclerosis; hyperostosis; osteoarthritis.

XX

OS Homo sapiens.

XX

PN US2002064832-A1.

XX

PD 30-MAY-2002.

XX

PF 14-MAR-2001; 2001US-0808972.

XX

XX

XX 03-MAY-1999; 99US-132250P.

XX

PR 10-NOV-1999; 99US-164463P.

XX

PR 04-FEB-2000; 2000US-180169P.

XX

PR 26-SEP-2000; 2000US-235295P.

XX

PR 03-MAY-2000; 2000US-0564595.

XX

PA (HART/) HART C E.

PA (TOPO/) TOPOUZIS S.

PA (GILB/) GILBERTSON D G.

XX

PI Hart CE, Topouzis S, Gilbertson DG;

XX

PI WPI; 2002-573696/61.

XX

DR

PT Reducing proliferation or extracellular matrix production by a cell in a mammal, useful for treating fibroproliferative disorders of bone, liver and kidney, comprises administering a zvegff4 antagonist

PT

Example 6; Page 24; 34pp; English.

XX

CC The present invention describes a method for reducing proliferation of or extracellular matrix production by a cell in a mammal. The method comprises administering to the mammal a composition comprising a therapeutically effective amount of a zvegff4 antagonist chosen from anti-zvegff4 antibodies, inhibitory polynucleotides, inhibitors of zvegff4 activation, and mitogenically inactive, receptor-binding variants of zvegff4. Zvegff4 (also called PDGF-D) is a multi-domain protein that is structurally related to platelet derived growth factor (PDGF) and vascular endothelial growth factors (VEGF). Zvegff4 has cystostatic, nephrotropic, hepatotropic, antiinflammatory, osteopathic and arthritic activities. The method is useful for reducing proliferation of mesangial, epithelial, endothelial, smooth muscle, fibroblast, osteoblast, osteoclast, neuronal, stromal, stellate or interstitial cells in a mammal, in particular proliferation of prostate tumour cells, and for reducing extracellular matrix production by a cell in a mammal suffering from a fibroproliferative disorder of kidney, bone or liver. In particular it is useful for reducing stellate cell activation. The method is useful for reducing metastasis of prostate cancer cells to bone in a mammal and for treating a fibroproliferative disorder of the kidney, liver or bone in a mammal. Fibroproliferative disorders of the kidney include, glomerulonephritis, diabetic glomerulosclerosis, lupus nephritis, renal arteriosclerosis and nephrotic syndrome, disorders of the liver include chronic active hepatitis and many other types of

CC cirrhosis, and disorders of the bone include osteopetrosis, hyperostosis, osteosclerosis, osteoarthritis, and ectopic bone formation in metastatic prostate cancer. The present sequence represents a human zvegff4 peptide, CC which is used in the preparation of polyclonal anti-peptide antibodies CC in an example from the present invention.

XX

XX SQ Sequence 24 AA;

XX

Query Match 33.8%; Score 33.5; DB 23; Length 24;

Best Local Similarity 58.3%; Pred. No. 84;

Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 3 PGH-ERMGRGT 13

DB 4 PGHRRGRAKT 15

XX

RESULT 14

ABP29938

ID ABP29938 standard; Peptide; 20 AA.

XX

AC ABP29938;

XX

DT 01-FEB-2002 (first entry)

XX

DE Peptide #2589 encoded by breast cell single exon nucleic acid probe.

XX

KW Human; microarray; single exon probe; gene expression; breast; disease; cancer.

XX

OS Homo sapiens.

XX

PN WO200157271-A2.

XX

PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US00662.

XX

XX

XX 04-FEB-2000; 2000US-0180312.

XX

PR 26-MAY-2000; 2000US-0207456.

XX

PR 30-JUN-2000; 2000US-0608408.

XX

PR 03-AUG-2000; 2000US-0632366.

XX

PR 21-SEP-2000; 2000US-0234687.

XX

PR 27-SEP-2000; 2000US-0236359.

XX

PR 04-OCT-2000; 2000GB-0024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

PA

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

PI WPI; 2001-496933/54.

XX

DR

PT New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes

PT

XX

PS Claim 27; SEQ ID NO 12906; 327pp + sequence listing; English.

XX

XX The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting CC the probes with a collection of detectably labelled nucleic acids CC derived from mRNA of human breast, and then measuring the label CC bound to each probe of the microarray. The probes are useful for CC verifying the expression of regions of genomic DNA predicted to CC encode proteins. They are useful for gene discovery, and for CC determining predisposition and/or prognosing breast disease. Gene CC expression analysis is useful for assessing the toxicity of chemical CC agents on cells. The microarray of this invention presents a far greater CC diversity of probes for measuring gene expression, with far less bias CC than expressed sequence tag microarrays. The method is suitable for CC rapid production of functional information from genomic sequence. The CC present sequence is a peptide encoded by a single exon nucleic acid



CC probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
SQ Sequence 20 AA;

Query Match 33.3%; Score 33; DB 22; Length 20;  
Best Local Similarity 58.3%; Pred. No. 85;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 8 MGRGRTSSKELA 19  
:||||| ||: |  
Db 5 VGRGRHCSKRTA 16

RESULT 15  
ABB35121  
ID ABB35121 standard; Peptide: 20 AA.  
XX  
AC ABB35121;  
XX

DE 04-FEB-2002 (first entry)  
XX

Peptide #2627 encoded by human foetal liver single exon probe.

Human: foetal liver; gene expression: single exon nucleic acid probe.

Homo sapiens.

WO200157277-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00669.

04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI: 2001-483447/52.

Human genome-derived single exon nucleic acid probes useful for

analyzing gene expression in human fetal liver -

Claim 27; SEQ ID NO 27756; 639pp + sequence listing; English.

The invention relates to a single exon nucleic acid probe for

measuring human gene expression in a sample derived from human foetal

liver. The single exon nucleic acid probes may be used for predicting,

measuring and displaying gene expression in samples derived from human

fetal liver. The present sequence is a peptide encoded by a single exon

nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
SQ Sequence 20 AA;

Query Match 33.3%; Score 33; DB 22; Length 20;  
Best Local Similarity 58.3%; Pred. No. 85;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
OY 8 MGRGRTSSKELA 19  
:||||| ||: |

Db 5 VGRGRHCSKRTA 16

RESULT 16  
AAM55944  
ID AAM55944 standard; Protein; 20 AA.  
XX

AC AAM55944;

DT 05-NOV-2001 (first entry)  
XX

Human brain expressed single exon probe encoded protein SEQ ID NO: 28049.

Human: brain expressed exon; gene expression analysis; probe;

microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

epilepsy; cancer.

Homo sapiens.

WO200157275-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00667.

04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI: 2001-483446/52.

Single exon nucleic acid probes for analyzing gene expression in human

brains -

Example 4; SEQ ID NO: 28049; 650pp + sequence listing; English.

The present invention provides a number of single exon nucleic acid

probes which are derived from genomic sequences expressed in the human

brain. They can be used to measure gene expressions in brain cell samples,

which may enable the diagnosis and improved treatment of nervous system

diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

epilepsy and cancers. The present sequence is a protein encoded by one of

the probes of the invention.  
SQ Sequence 20 AA;

Query Match 33.3%; Score 33; DB 22; Length 20;  
Best Local Similarity 58.3%; Pred. No. 85;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 8 MGRGRTSSKELA 19  
:||||| ||: |  
Db 5 VGRGRHCSKRTA 16

RESULT 17  
AAM68310  
ID AAM68310 standard; Protein; 20 AA.  
XX  
AC AAM68310;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28616.  
XX

KW Human; bone marrow expressed exon; gene expression analysis; probe;  
KM microarray; cancer; leukaemia; lymphoma; myeloma.  
XX  
OS Homo sapiens.  
XX  
PN WO200157276-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00668.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
(MOLE-) MOLECULAR DYNAMICS INC.  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488900/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for  
XX analyzing gene expression in human bone marrow -  
PS Example 4; SEQ ID NO: 28616; 658bp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
CC protein encoded by one of the probes of the invention.  
XX  
SQ Sequence 20 AA:  
XX  
Query Match 33.3%; Score 33; DB 22; Length 20;  
Best Local Similarity 58.3%; Pred. No. 85;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
OY 8 MGRGRTSKELA 19  
XX :||||| ||: |  
DB 5 VGRGRHCSKRTA 16  
XX  
RESULT 18  
ID AAM03860  
XX AAM03860 standard; Protein: 20 AA.  
XX  
AC AAM03860;  
XX  
DT 09-OCT-2001 (first entry)  
XX  
DE Peptide #2542 encoded by probe for measuring breast gene expression.  
XX  
KW Probe; human; breast disease; breast cancer; development disorder;  
KM inflammatory disease; proliferative breast disease; non-carcinoma tumour.  
XX  
OS Homo sapiens.  
XX  
PN WO200157270-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 29-JAN-2001; 2001WO-US00661.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
FA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
PN WPI; 2001-476286/51.  
XX  
DR Novel single exon nucleic acid probe used to measuring gene expression  
XX in a human breast -  
PT  
PS Claim 27; SEQ ID NO 12600; 322pp; English.  
XX  
CC The present invention relates to novel single exon nucleic acid probes  
CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for measuring human gene expression in  
CC a human breast sample, where the probe hybridises at high stringency to a  
CC nucleic acid expressed in the human breast. The probes are useful for  
CC predicting, diagnosing, grading, staging, monitoring and prognosing  
CC diseases of the human breast, particularly those diseases with polygenic  
CC aetiology. The diseases include: breast cancer, disorders of development,  
CC inflammatory diseases of the breast, fibrocystic changes, proliferative  
CC breast disease and non-carcinoma tumours.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 20 AA:  
XX  
Query Match 33.3%; Score 33; DB 22; Length 20;  
Best Local Similarity 58.3%; Pred. No. 85;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
OY 8 MGRGRTSKELA 19  
XX :||||| ||: |  
DB 5 VGRGRHCSKRTA 16  
XX  
RESULT 19  
ID ABG37860  
XX ABG37860 standard; Peptide: 20 AA.  
XX  
AC ABG37860;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 27525.  
XX  
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
KW chronic obstructive pulmonary disease; interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
KW primary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200186003-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00665.  
XX  
PR 04-FEB-2000; 2000US-180312P.  
PR 26-MAY-2000; 2000US-207456P.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-234687P.





CC The proteins are useful in the diagnosis, detection and treatment of  
CC diseases and/or disorders associated with aberrant uteroglobin-like  
CC activity, such as inflammatory disorders (glomerulonephritis, rheumatoid  
CC arthritis, autoimmune disorders e.g., multiple sclerosis, Grave's  
CC disease); respiratory disorders (allergy, asthma); immune deficiency  
CC diseases (leukemia, sepsis, acne, psoriasis); cancers (adenocarcinoma);  
CC gastrointestinal disorders (inflammatory bowel disease); immunologic  
CC deficiency syndromes (DiGeorge syndrome, HIV infection); haematopoietic  
CC disorders, transplantation rejections (graft-versus-host disease);  
CC hyperproliferative disorders (neoplasm, Gaucher's disease);  
CC cardiovascular diseases (arrhythmias); cerebrovascular diseases  
CC (thrombosis); sex-linked disorders, for treating infectious agents,  
CC tumours, uveitis, atherosclerosis, ulcers, as birth control agent, wound  
CC healing, and for treating neurodegenerative and behavioural disorders  
CC (e.g., Alzheimer's disease, Parkinson's disease, Hartnup disease, mania,  
CC autism). Uteroglobin-like proteins and antibodies are useful as reagents  
CC for differential identification of tissues or cell types present in a  
CC biological sample. They are also used as immunological probes for  
CC differential identification of tissues. The polynucleotides of the  
CC invention are useful in gene therapy, for chromosome identification.  
CC The present sequence represents a human uteroglobin-like protein HFCB041  
CC fragment of the invention.

SQ Sequence 17 AA;

Query Match 32.3%; Score 32; DB 22; Length 17;

Best Local Similarity 55.6%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;OY 3 PGERMGRG 11  
1 1 1 1 1  
DB 9 PHEHMGPG 17

RESULT 24

AAR04485

ID: AAR04485 standard; protein: 18 AA.

XX AAR04485;

XX 20-SEP-1990 (first entry)

XX Human immunodeficiency virus hybrid peptide RP113.

XX Hybrid peptide RP113; therapy; AIDS; principal neutralising domain;

XX antibodies; diagnosis; prophylaxis.

XX Synthetic.

XX WO9003984-A.

XX 19-APR-1990.

XX 29-SEP-1989; 89WO-US04302.

XX 19-SEP-1989; 89US-0407663, US-252949; WO-U04302.

XX (REPL-) REPLIGEN CORP.

XX Rusche JR, Putney SD, Javaherian K, Farley J, Grimalia R, Lynn D;  
XX Petro-Breyer J;

XX WPI: 1990-147824/19.

XX Principal neutralising domain of HIV variants - used for producing  
XX peptide(s) and antibodies for diagnosis; prophylaxis; and/or therapy  
XX of HIV infection.

XX Claim 8 (88); page 77; 108pp; English.

XX Peptide RP113 comprises segments of the Principal Neutralising Domain  
XX (envelope protein) from a HIV isolate.  
XX The last Cys residue is added for the purpose of crosslinking

CC to carrier proteins. Cysteine residues may be added, so that the  
CC residues at or near both ends form a disulfide bond, giving peptide a  
CC loop-like configuration, which can be utilized to enhance immunogenic  
CC properties of the peptides. Protein is capable of eliciting, and/or  
CC binding with, neutralising antibodies. The neutralising domain is bounded  
CC by cysteine residues which occur at positions 296 and 331. The peptides  
CC can be used as immunogens or screening reagents to generate or identify  
CC poly- or monoclonal antibodies.  
CC See also AAR04427-R04506 and AAR04273-Q04279.

SQ Sequence 18 AA;

Query Match 32.3%; Score 32; DB 11; Length 18;

Best Local Similarity 60.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;OY 3 PGERMGRGR 12  
1 1 1 1 1  
DB 4 PGRMRGRGR 13

RESULT 25

AAM72540

ID: AAM72540 standard; protein: 19 AA.

XX AAM72540;

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed probe encoded protein SEQ ID NO: 32846.

XX Human; bone marrow expressed exon; gene expression analysis; probe;

XX microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00668.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI: 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for  
XX analyzing gene expression in human bone marrow -  
XX Example 4; SEQ ID NO: 32846; 658bp + Sequence Listing; English.  
XX The present invention provides a number of single exon nucleic acid  
XX probes which are derived from genomic sequences expressed in the human  
XX bone marrow. They can be used to measure gene expression in bone marrow  
XX samples, which may enable the improved diagnosis and treatment of cancers  
XX such as lymphoma, leukemia and myeloma. The present sequence is a  
XX protein encoded by one of the probes of the invention.

SQ Sequence 19 AA;

Query Match 32.3%; Score 32; DB 22; Length 19;

Best Local Similarity 46.2%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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OY 3 PGHERMGRRSS 15  
| | : | | | |  
Db 3 PQRRHLEGLDSS 15

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job time : 54 secs